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OM nucleic - nucleic search, using sw model

Run on: September 16, 2004, 17:59:08 ; Search time 596 Seconds
(without alignments)
9967.860 Million cell updates/sec

Title: US-10-063-736-129

Perfect score: 1177

Sequence: 1 aacttctacatggcctcct.....ataaccacacatggcaaaaa 1177

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3327077 seqs, 2523723180 residues

Total number of hits satisfying chosen parameters: 6654154

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
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- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
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- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq2:*
- 14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1177	100.0	1177	13	US-10-206-915-381
2	1177	100.0	1177	13	US-10-199-670-381
3	1177	100.0	1177	13	US-10-201-858-381
4	1177	100.0	1177	13	US-10-081-056-271
5	1177	100.0	1177	13	US-10-219-535-211
6	1177	100.0	1177	13	US-10-232-230-211
7	1177	100.0	1177	13	US-10-205-890-381
8	1177	100.0	1177	13	US-10-208-024-381
9	1177	100.0	1177	13	US-10-201-853-381
10	1177	100.0	1177	13	US-10-063-745-129
11	1177	100.0	1177	13	US-10-063-512-129
12	1177	100.0	1177	13	US-10-063-513-129
13	1177	100.0	1177	13	US-10-063-569-129
14	1177	100.0	1177	13	US-10-063-551-129

15	1177	100.0	1177	13	US-10-174-581-381	Sequence 381, App
16	1177	100.0	1177	13	US-10-176-483-381	Sequence 381, App
17	1177	100.0	1177	13	US-10-176-749-381	Sequence 381, App
18	1177	100.0	1177	13	US-10-176-914-381	Sequence 381, App
19	1177	100.0	1177	13	US-10-176-915-381	Sequence 381, App
20	1177	100.0	1177	13	US-10-063-555-129	Sequence 129, App
21	1177	100.0	1177	13	US-10-063-563-129	Sequence 129, App
22	1177	100.0	1177	13	US-10-063-594-129	Sequence 129, App
23	1177	100.0	1177	13	US-10-063-553-129	Sequence 129, App
24	1177	100.0	1177	13	US-10-063-554-129	Sequence 129, App
25	1177	100.0	1177	13	US-10-176-484-381	Sequence 381, App
26	1177	100.0	1177	13	US-10-180-550-381	Sequence 381, App
27	1177	100.0	1177	13	US-10-183-014-381	Sequence 381, App
28	1177	100.0	1177	13	US-10-187-738-381	Sequence 381, App
29	1177	100.0	1177	13	US-10-187-740-381	Sequence 381, App
30	1177	100.0	1177	13	US-10-187-883-381	Sequence 381, App
31	1177	100.0	1177	13	US-10-194-363-381	Sequence 381, App
32	1177	100.0	1177	13	US-10-194-460-381	Sequence 381, App
33	1177	100.0	1177	13	US-10-194-463-381	Sequence 381, App
34	1177	100.0	1177	13	US-10-194-484-381	Sequence 381, App
35	1177	100.0	1177	13	US-10-195-884-381	Sequence 381, App
36	1177	100.0	1177	13	US-10-195-896-381	Sequence 381, App
37	1177	100.0	1177	13	US-10-196-744-381	Sequence 381, App
38	1177	100.0	1177	13	US-10-196-755-381	Sequence 381, App
39	1177	100.0	1177	13	US-10-196-757-381	Sequence 381, App
40	1177	100.0	1177	13	US-10-197-704-381	Sequence 381, App
41	1177	100.0	1177	13	US-10-197-710-381	Sequence 381, App
42	1177	100.0	1177	13	US-10-198-758-381	Sequence 381, App
43	1177	100.0	1177	13	US-10-198-766-381	Sequence 381, App
44	1177	100.0	1177	13	US-10-199-304-381	Sequence 381, App
45	1177	100.0	1177	13	US-10-199-309-381	Sequence 381, App

ALIGNMENTS

RESULT 1
US-10-206-915-381
; Sequence 381, Application US/10206915
; Publication No. US20040029221A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Deschuyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C513
; CURRENT APPLICATION NUMBER: US/10/206,915
; CURRENT FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28

Query Match	100.0.%;	Score 1177;	DB 13;	Length 1177;
Best local Similarity	100.0.%;	Pred. No. 9..7e-305;		
Matches 1177;	Conservative 0;	Mismatches 0;	Gaps 0;	
Qy	1	AACCTTCATCATGGCCCTCCTGCGTGTGCTCTTCTCAGCCTCCTGCCGCTGCCTAC	60	
Dd	1	AACCTTCATCATGGCCCTCCTGCTGCTGTGCTCTTCTCAGCCTCCTGCCGCTGCCTAC	60	
Qy	61	ACCATCATGTCCCTCCCAACCTCTTTTGACTCGGGCCGTTTAGGTGCGAGTCTCAGTT	120	
Dd	61	ACCATCATGTCCCTCCCAACCTCTTTTGACTCGGGCCGTTTAGGTGCGAGTCTCAGTT	120	
Qy	121	GCCGGGAGCACCTCCCTCCGAGGCAGTCTGCTCAGAGGGGCTCGGCCAGAAATCCA	180	
Dd	121	GCCGGGAGCACCTCCCTCCGAGGCAGTCTGCTCAGAGGGGCTCGGCCAGAAATCCA	180	
Qy	181	GTTCCTGGTTTCATGCCAGCTGTAAAAGGCCATGGAACTTTGGTGAATACCGATGCCA	240	
Dd	181	GTTCCTGGTTTCATGCCAGCTGTAAAAGGCCATGGAACTTTGGTGAATACCGATGCCA	240	
Qy	241	TTTTAAGAGGGTTTTCTGCCAGGATGGAATGTTAGGTGCTGCTGCTGCGCTGTTCAAT	300	
Dd	241	TTTTAAGAGGGTTTTCTGCCAGGATGGAATGTTAGGTGCTGCTGCTGCGCTGTTCAAT	300	
Qy	301	TTCAGTAGCCACGACCCACCTGTGGCCGTTGAGTGTCTGAAATGAGAACTGAGAAAAAT	360	
Dd	301	TTCAGTAGCCACGACCCACCTGTGGCCGTTGAGTGTCTGAAATGAGAACTGAGAAAAAT	360	
Qy	361	AAHTTCTCATGTATTTTCTCATTTATTTATTAATTTTAACTGATAGTGTGATCATTTT	420	
Dd	361	AAHTTCTCATGTATTTTCTCATTTATTTATTAATTTTAACTGATAGTGTGATCATTTT	420	
Qy	421	GGGGTACATGTGATAATTGGATACATGTATACAATATATAATGATCAAAATCAGGTAAC	480	
Dd	421	GGGGTACATGTGATAATTGGATACATGTATACAATATATAATGATCAAAATCAGGTAAC	480	
Qy	481	TGGGATATCAATCACATCAAACATTTATTTTTTATTTCTTTTATGACAGAGTCTCACTCTG	540	
Dd	481	TGGGATATCAATCACATCAAACATTTATTTTTTATTTCTTTTATGACAGAGTCTCACTCTG	540	
Qy	541	TCACCCAGGCTGGAGTCAGTGGTGCCATCTCAGCTTACTGCAACTCTCCCTGCCAGGT	600	
Dd	541	TCACCCAGGCTGGAGTCAGTGGTGCCATCTCAGCTTACTGCAACTCTCCCTGCCAGGT	600	
Qy	601	TCAAGCAATCTCATGCTCCACTCCCAAGTAGCTGGGACTACAGGCATGCAACCAAT	660	
Dd	601	TCAAGCAATCTCATGCTCCACTCCCAAGTAGCTGGGACTACAGGCATGCAACCAAT	660	
Qy	661	GCCCAACTAATTTTTGTATTTTAGTAGAGACGGGTTTTGCCATGTTGCCAGGCTGGC	720	
Dd	661	GCCCAACTAATTTTTGTATTTTAGTAGAGACGGGTTTTGCCATGTTGCCAGGCTGGC	720	
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Dd	721	CTTGAACTCCTGGGCTCAAAACATCCACTTGCCTCGGCCCTCCCAAGTGTATGATTACA	780	
Qy	781	GGCGTAGCCACCGTGCTGCCCTAAACATTTATCTTTCTTTGTGTGGAACTTTGAA	840	
Dd	781	GGCGTAGCCACCGTGCTGCCCTAAACATTTATCTTTCTTTGTGTGGAACTTTGAA	840	
Qy	841	ATTATACAATGAATTTATGTTAACTGTCATCTCCCTGCTGTATGGAACACTGGGACT	900	
Dd	841	ATTATACAATGAATTTATGTTAACTGTCATCTCCCTGCTGTATGGAACACTGGGACT	900	
Qy	901	TCTTCCCCTCTATCTAACTGATATATTTGTAACAGTTTAAACCAACCGTACTCATCCCCACTC	960	
Dd	901	TCTTCCCCTCTATCTAACTGATATATTTGTAACAGTTTAAACCAACCGTACTCATCCCCACTC	960	
Qy	961	CTCTCTATCCTTCCCAACCTCTGATCACTCATTTCTACTCTCTACTCTCAATGAGATCCAC	1020	
Dd	961	CTCTCTATCCTTCCCAACCTCTGATCACTCATTTCTACTCTCTACTCTCAATGAGATCCAC	1020	
Qy	1021	TTTTTTAGCTCCCATGTGAGTAAGAAAAATGCAATATTTGTCTTTCTGTGCGCTGGCTTA	1080	

Db	1021	TTTTTAGCTCCCAACATGTGAGTAAGAAAAATGCAATATTTTCTCTTTCTGTCCTGGCTTA	10890
Qy	1081	TTTCACATTACATAATGACATCTCTGTTCCATCCATGTTGTCGAAATGACAGGATTTTCGT	1140
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Qy	1141	TCTTAATTTCAAATTAATAATACACACATGCGAAAAA	1177
Db	1141	TCTTAATTTCAAATTAATAATACACACATGCGAAAAA	1177

RESULT 3

US-10-201-858-381

; Sequence 381, Application US/10201858

; Publication No. US20040038337A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3430R1C464

; CURRENT APPLICATION NUMBER: US/10/201,858

; CURRENT FILING DATE: 2002-07-23

; PRIOR APPLICATION NUMBER: 16/052586

; PRIOR FILING DATE: 2002-01-15

; PRIOR APPLICATION NUMBER: 60/059263

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/059266

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/063120

; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/063121

; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/063486

; PRIOR FILING DATE: 1997-10-21

; PRIOR APPLICATION NUMBER: 60/063540

; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/063541

; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/063544

; PRIOR FILING DATE: 1997-10-28

; Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 381

; LENGTH: 1177

; TYPE: DNA

; ORGANISM: Homo Sapien

US-10-201-858-381

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	Matches 1177	Conservative 0	Mismatches 0		
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DB	1	AACCTTCACATGCGCCCTCCTGCTGCTGCTCTCTCTCAGCTCTCTGCGGTGGCCCTAC	60		
QY	61	ACCATCATGTCCCTCCCAACCTCTCTTTGACATGCGGGCGGTTTCAGGTGCAGAGTCTCAGTT	120		
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 781 GGGGTAGGACCGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 840
 781 GGGGTAGGACCGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 840
 841 ATTATCAATGAATTAATTTGTATTTGTATTTGTATTTGTATTTGTATTTGTATTTGTATTT 900
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 901 TCTTCCCTCTATCTAATGATATTTGTACAGTTTAAACCGATTAACCGATTAACCGATTAAC 960
 961 CTCTCTATCTTCCCAACCTCTGATCACTCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1020
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 1021 TTTTGTAGTCCACATGTAGTAAAGAAATGAATGAATGAATGAATGAATGAATGAATGAATGA 1080
 1021 TTTTGTAGTCCACATGTAGTAAAGAAATGAATGAATGAATGAATGAATGAATGAATGAATGA 1080
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 1141 TCTTAATTTCAATTAATAATCAACATGGGCAAAA 1177
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RESULT 4
 US-10-081-056-271
 ; Sequence 271, Application US/10081056
 ; Publication No. US20040043927A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Marsters, Scot A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Stephan, Jean-Philippe F.
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Williams, P.Mickey
 ; APPLICANT: Ye, Weilan
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
 ; TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
 ; FILE REFERENCE: P3235F1C1
 ; CURRENT APPLICATION NUMBER: US/10/081,056
 ; PRIOR FILING DATE: 2002-02-20
 ; PRIOR APPLICATION NUMBER: PCT/US01/21735
 ; PRIOR FILING DATE: 2001-07-09
 ; PRIOR APPLICATION NUMBER: US 60/219,556
 ; PRIOR FILING DATE: 2000-07-20
 ; PRIOR APPLICATION NUMBER: US 60/220,624
 ; PRIOR FILING DATE: 2000-07-25
 ; PRIOR APPLICATION NUMBER: US 60/220,664
 ; PRIOR FILING DATE: 2000-07-25
 ; PRIOR APPLICATION NUMBER: PCT/US00/20710
 ; PRIOR FILING DATE: 2000-07-28
 ; PRIOR APPLICATION NUMBER: US 60/222,695
 ; PRIOR FILING DATE: 2000-08-02
 ; PRIOR APPLICATION NUMBER: US 09/643,657
 ; PRIOR FILING DATE: 2000-08-17
 ; PRIOR APPLICATION NUMBER: PCT/US00/23522
 ; PRIOR FILING DATE: 2000-08-23
 ; PRIOR APPLICATION NUMBER: PCT/US00/23328
 ; PRIOR FILING DATE: 2000-08-24
 ; PRIOR APPLICATION NUMBER: US 60/230,978
 ; PRIOR FILING DATE: 2000-09-07
 ; PRIOR APPLICATION NUMBER: US 60/000,000
 ; PRIOR FILING DATE: 2000-09-15
 ; PRIOR APPLICATION NUMBER: US 09/664,610
 ; PRIOR FILING DATE: 2000-09-18
 ; PRIOR APPLICATION NUMBER: US 09/665,350
 ; PRIOR FILING DATE: 2000-09-18
 ; PRIOR APPLICATION NUMBER: US 60/242,922
 ; PRIOR FILING DATE: 2000-10-24
 ; PRIOR APPLICATION NUMBER: US 09/709,238
 ; PRIOR FILING DATE: 2000-11-08
 ; PRIOR APPLICATION NUMBER: PCT/US00/30952
 ; PRIOR FILING DATE: 2000-11-08
 ; PRIOR APPLICATION NUMBER: PCT/US00/30873
 ; PRIOR FILING DATE: 2000-11-10
 ; PRIOR APPLICATION NUMBER: PCT/US00/32678
 ; PRIOR FILING DATE: 2000-12-01
 ; PRIOR APPLICATION NUMBER: US 09/747,259
 ; PRIOR FILING DATE: 2000-12-20
 ; PRIOR APPLICATION NUMBER: PCT/US00/34956
 ; PRIOR FILING DATE: 2000-12-20
 ; PRIOR APPLICATION NUMBER: US 09/767,609
 ; PRIOR FILING DATE: 2001-01-22
 ; PRIOR APPLICATION NUMBER: US 09/796,498
 ; PRIOR FILING DATE: 2001-02-28
 ; PRIOR APPLICATION NUMBER: PCT/US01/06520
 ; PRIOR FILING DATE: 2001-02-28
 ; PRIOR APPLICATION NUMBER: PCT/US01/06666


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Db 121 GCCGGGAGCACCTCCCTCCGAGGAGTCTGCTCAGAGGCGCTCGGCCAGAAATCCA 180
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QY 241 TTTAAGAGGTTTCTGCCAGAGTGAATAAGTTAGGTGCTTCTGCTGCGCTGTTTCAT 300
Db 241 TTTAAGAGGTTTCTGCCAGAGTGAATAAGTTAGGTGCTTCTGCTGCGCTGTTTCAT 300
QY 301 TTCAGTACCCAGCCAGCACCTGTGGCCGTTGAGTGTGTTGAAATGAGGAACCTGAGAAATTT 360
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QY 361 AATTCTCATGATTTTCTCATTTATTTATTTATTTATTTTATTTTATTTTATTTTATTTT 420
Db 361 AATTCTCATGATTTTCTCATTTATTTATTTATTTATTTTATTTTATTTTATTTTATTTT 420
QY 421 GGGGTACATGTGATTTTGGATACATGTATACAAATATATATATATATATATATATATATAT 480
Db 421 GGGGTACATGTGATTTTGGATACATGTATACAAATATATATATATATATATATATATATAT 480
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Db 781 GCGGTGAGCCACCGTGCCTGAGTAAACATTTATTTATTTATTTATTTATTTATTTATTT 840
QY 841 ATTATACAAATGAAATTTATTTTAACTGTATCTCCCTGCTGTGCTATGGAACATGGACT 900
Db 841 ATTATACAAATGAAATTTATTTTAACTGTATCTCCCTGCTGTGCTATGGAACATGGACT 900
QY 901 TCTTCCCTCTATCTAATCTGATATTTGACAGTAAACCAACCGTACTTTCATCCCACTC 960
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QY 1081 TTTCACTTAAATATGATCTTCTGTTCCATCCATGTTGCTGGAATGACAGGATTTTCTG 1140
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QY 1141 TCTTAATTTCAATTAATAAACCACATGCAAAAA 1177
Db 1141 TCTTAATTTCAATTAATAAACCACATGCAAAAA 1177
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; Sequence 381, Application US/10201853
; Publication No. US20040053358A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430RIC465
; CURRENT APPLICATION NUMBER: US/10/201,853
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 381
; LENGTH: 1177
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-201-853-381
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Best Local Similarity 100.0%; Pred. No. 9.7e-305;
Matches 1177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACTTCTACATGGGCGCTCCTGCTGTGTGCTCTTCTCCTCAGCCTCCTGCCGTGGCCTAC 60
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QY 181 GTTCTGGTTTCATGCCAGCCTGTAAGGCCCATGGAACCTTTGGGTGAATCACCAGATCCA 240
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Db 781 GCGTGGAGCCACCGTGGCTTAACTGCTATCTCCCTGCTGTGCTATGGAACCTTTGAA 840
Qy 841 ATTATACATGAAATTTATTTAACTGCTATCTCCCTGCTGTGCTATGGAACCTTTGAA 900
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Db 1141 TCTTAAATTTCAATTTAAATTAACCAACATGCAATGCAATGCAATGCAATGCAAT 1177

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; Sequence 129, Application US/10063551
; Publication No. US20020183494A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,551
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 129
; LENGTH: 1177
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-063-551-129

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Query Match      100.0%; Score 1177; DB 13; Length 1177;
Best Local Similarity 100.0%; Pred. No. 9, 7e-305;
Matches 1177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AACTTCTACATGGGCTCTCTGCTGCTGGTGTCTTCTCCTCAGCCTCTCGCGGTGGCTAC 60
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Qy 61 ACCATCATGTCCCTCCACCCCTCTTGTGACTGGGGCCGTTGAGTGCAGAGTCTCAGTT 120
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Qy 121 GCCCGGAGCACCTCCCTCCGAGGAGCTGCTCCTCAGAGGCGCTCGGCCAGAAATTCOA 180
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Qy 181 GTTCTGTTTCATGCCAGCCTGTAAAGGCCATGGAACCTTTGGGTGAATCAGCGATGCCA 240
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Qy 241 TTTAAGAGGGTTTCTGCGAGGATGGAATGTTAGGTGTTCTGTGCTGCGCTGTTTCAT 300
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Qy 541 TCACCCAGGCTGGAGTGAGTGCGCATCTCAGCTTACTGCAACCTCTGCTGCCAGGT 600
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; PRIOR APPLICATION NUMBER: 60/083559
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/084366
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; PRIOR FILING DATE: 1998-06-02
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; PRIOR FILING DATE: 1998-06-09
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; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088826
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Best Local Similarity 100.0%; Pred. No. 9.7e-305;
Matches 1177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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GenCore version 5.1.6
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Perfect score: 1177
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Total number of hits satisfying chosen parameters: 1365418

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	252.8	21.5	12047	4	US-09-474-629-11
4	252.8	21.5	12047	4	US-09-151-376-3
C 5	233.8	19.9	99916	4	US-09-816-095-3
C 6	233	19.8	313	4	US-09-621-976-13292
C 7	232.4	19.7	22976	4	US-09-269-939A-19
C 8	232.4	19.7	23187	4	US-09-499-522-1
C 9	231.2	19.6	99500	4	US-09-798-056-10
C 10	229.2	19.5	246240	2	US-08-724-394A-20
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C 15	228.2	19.4	21721	4	US-09-269-939A-41
C 16	227.8	19.4	21968	4	US-09-851-985-3
C 17	227.2	19.3	48763	4	US-09-916-204-3
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C 20	226.4	19.2	2457	4	US-09-620-312D-223
C 21	226.2	19.2	80246	3	US-09-078-294-4
C 22	225	19.1	399	4	US-09-621-976-13959
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ALIGNMENTS

RESULT 1
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; Sequence 1, Application US/09022461
; Patent No. 5964371
; GENERAL INFORMATION:
; APPLICANT: HENDERSON, Daniel R.
; APPLICANT: SCHUUR, Eric R.
; APPLICANT: LAMPARSKI, Henry G.
; APPLICANT: YU, De Chao
; TITLE OF INVENTION: PROSTATE CANCER DRUG SCORE
; TITLE OF INVENTION: ENING
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,461
; FILING DATE: 12-FEB-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/906,192
; FILING DATE: 04-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Catherine, Polizzi M
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 34802-20003.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-813-5600
; TELEFAX: 415-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12047 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-022-461-1

Query Match 21.5%; Score 252.8; DB 2;
Best Local Similarity 64.2%; Pred. No. 3, 1e-61;
Matches 429; Conservative 0; Mismatches 232; Indels 7; Gaps 3;


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Qy      1138 CGTCTTA 1145
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Db      2392 ATTITCA 2399

RESULT 4
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; Sequence 3, Application US/09151376
; Patent No. 6676935
; GENERAL INFORMATION:
; APPLICANT: Henderson, D.R.
; APPLICANT: Schuur, E.R.
; TITLE OF INVENTION: TISSUE SPECIFIC VIRAL VECTORS
; FILE REFERENCE: 348022000221
; CURRENT APPLICATION NUMBER: US/09/151,376
; CURRENT FILING DATE: 1998-09-10
; EARLIER APPLICATION NUMBER: 08/669,753
; EARLIER FILING DATE: 1996-06-26
; EARLIER APPLICATION NUMBER: 08/495,034
; EARLIER FILING DATE: 1995-06-27
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; SOFTWARE: PatentIn Ver. 2.0
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Query Match	21.5%	Score 252.8	DB 4	Length 12047
Best Local Similarity	64.2%	Pred. No. 3.1e-61		
Matches 429	Conservative 0	Mismatches 232	Indels 7	Gaps 3
QY	478	AATGGGATATCCATCACATCAACATATTTATTTTTATTTCTTTTTAGACAGAGTCTCACT	537	
Db	1739	AAATGGTCTCCTCACATTTATTTATTTATATATTTATTTAGTTTTTGAGATGGAGCCTCGCT	1798	
QY	538	CTGTCAACCCAGGCTGAGTGCAGTGTGCATCTCAGCTTACTGCAACCTCTGCCTGCCA	597	
Db	1799	CTGTCTCTTAGGCTGGAGTGCATATAGTGGATACCA-CTCATCTGCAACCTCTGCTCTCTC	1857	
QY	598	GGTTCAAGCGATTCATCGCTCCACTCCCAAGTAGCTGGGACTCAGGCAATGCACCCAC	657	
Db	1858	TGTTCAAGTGATTTTCTTACCTCAGCCTCCGAGTAGCTGGGATTCAGGTGCGTGCCAC	1917	
QY	658	AATGCCCAACTAAATTTTCTATTTTATTTAGTAGAGAGGGGTTTGCCATGTTGCCAGGCT	717	
Db	1918	CACACCGGCTAAATTTTGTATTTTGTATTTTGTAGAGAGGGGTTTGCCATGTTGCCAGGCT	1977	
QY	718	GGCCTTTGAACCTCGTCGCCCTCAAACAATCCACATTCGCCTCGGCCCTCCCAAAGTGTATGATT	777	
Db	1978	GGTCTTTGAACCTCTGCATCAGGTGATCCACCTGCGCTTGGCCTCCTAAAGTGTGGGATT	2037	
QY	778	ACAGGCGTGAGCCACCGTGCCTGGCCTAAACATTTATCTTTTCTTTGTGTGGGAACTTT	837	
Db	2038	ACAGGATGAGCCACCGTGCCTGCCAACCACTTTATTTATTTTATTTTATTTTAAATTT	2097	
QY	838	GAAATATACAATGAATTTATTTAACTGTCATCTCCCTGCTGTGTATGGAACACTGGG	897	
Db	2098	CAGCTTCTATTTGAANAACAGGGGCACATATATAGGAT-IGTTACATGGGTATATTGA	2155	
QY	898	ACTTCTTCCTCTATCTACTGATATATTTGTACCAGTTAACCAACCGTACTTCATCCCCA	957	
Db	2156	ACTCAGGTAGTGATCATACTACCCACAGTAGGTTT-----CAACCCACTCCCCCTCTT	2211	
QY	958	CTCCTCTCTATCCTTCCCAACCTCTGATCACCTCATTTCTACTCTCTACCTCCATGAGATC	1017	
Db	2212	TTCCCTCCCATTTCTAGTAGTGTGCAGTGTCATTGTTCTCATGTTTATGCTATGTGTGC	2271	
QY	1018	CACTTTTTTAGTCCCAATGTGAGTAAAGAAATATTTGTCTTTCTGTGCGCTGGC	1077	
Db	2272	TCAGGTTTAGTCCCACTCTAAAGTGAGAACGTGTGGTATTTGATTTTCTGTGCCCTGTG	2331	

Db 2332 TTAATTCATTAGGATTATGGCTCCAGCTCCATTTCATATTGCTGTAAGGATATGATTC 2391
QY 1138 CGTTCCTTA 1145
Db 2392 ATTTTCA 2399
RESULT 5
US-09-816-095-3/c
; Sequence 3, Application US/09816095
; Patent No. 6664084
; GENERAL INFORMATION:
; APPLICANT: GAN, Weinliu
; TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES
; FILE REFERENCE: CLO01147
; CURRENT APPLICATION NUMBER: US/09/816.095
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 9916
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(9916)
; OTHER INFORMATION: n = A,T,C or G
US-09-816-095-3

Query Match 19.9%; Score 233.8; DB 4; Length 9916;
Best Local Similarity 62.3%; Pred. No. 2.5e-55;
Matches 417; Conservative 0; Mismatches 247; Indels 5; Gaps 3;
QY 504 TTTATTTTCTTTTATTTAGACAGAGTCTCACTCTGTGACCCAGGCTGGAGTGCAGTGG 563
Db 48717 TGTCTTTCTTTTGTGAGACGGAGTCTTGTCTTGTGCCCAGGCTGGAGTGCAGTGG 48658
QY 564 TGCATCTCAGCTTACTGCACACTCTGCTGCGAGTTCAGAGTCTCATGCTCCAC 623
Db 48657 CATGATCTCAGCTCACTGCAAGCTCCACCTCCGAGTTCATGCCATCTCTGCTCAGT 48598
QY 624 CTCCTCAAGTACCTGGAGTACAGGCTGACCAACAAATGCCCACTAA- TTTTGTATTTT 682
Db 48597 CTCCTGAGTACCTGGAGTCAAAAGCCACACACACCGGCTAATTTTGTATTTT 48538
QY 683 TAGTAGACACGGGTTTGGCATGTTGCCAGGCTGGCTTGAATCTCTGGCTCAACA 742
Db 48537 TAGTAGAGATGGGTTTCCACCGTGTGGCCAGGATGCTCAATCTCTGACCTC-CTG 48480
QY 743 ATCCACTTGCCTCGGCTCCCAAGTGTATGATTACAGGCTGAGCCACCGCTGCTGGC 802
Db 48479 ATCCACCGCTCTAGCTTCCAAAGTGTGGATTAAGCGGTGAGCCATGTGCGCGC 48420
QY 803 CTAACAATTAATCTTTTCTTGTGTGGAACTTTGAAATATACAAATGAAATATGTTTA 862
Db 48419 CCCTCTCTTTTAAAGACTTTATTTAGGTTTCCAGGGTCCATGTGCAAGTTTGTATC 48360
QY 863 ACTGTCATCTCCCTGCTGTGCTATGGAACACTGGACTTCTTCCCTCTATCTAATCTAT 922
Db 48359 AATAAATTGCATGTTGTGGGGTTTGTGTACAGATTTTCAACCCAGGTAATAGCAT 48300
QY 923 ATTTGTACAGTTAAACCAACCGTACTTATCCCACTCTCTCTATCTTCTCCCAACCTCT 982
Db 48299 ATTAGTCAATTTTCT 48240
QY 983 GATCACCCTACTCTACTCTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1042
Db 48239 GTCCA--TTATTCCTCTTTTGTATCCATGTTTCTCAATGTTTGTCTTCCACTTAAG 48182
QY 1043 TAAGAAAATGCAATATTTGCTCTTTCTGTGCTGCTTATTTCACTTAACATAATGACTTC 1102

Db 48181 TTAGAACATGAGCAGCAATTTGGTTTCTGTCTCTACATTAGTTCGTTAGATTGACCTC 48122
QY 1103 CTGTTCCATCCATGTTGCTGCAAAATGACAGGATTCGTTCTTAATTTCAATAAATAAC 1162
Db 48121 CAGCACTATCCATGTTGCTGCAAAAGGACATCATCTTATTTCTTTTATGTTTACGTAGT 48062
QY 1163 CACACATGG 1171
Db 48061 ATTACATGG 48053
RESULT 6
US-09-621-976-13292/c
; Sequence 13292, Application US/09621976
; Patent No. 6639083
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 13292
; LENGTH: 313
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-13292

Query Match 19.8%; Score 233; DB 4; Length 313;
Best Local Similarity 84.0%; Pred. No. 1.6e-56;
Matches 263; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
QY 511 TTTATTTCTTTTATGACAGAGTCTCACTCTGTGACCCAGGCTGGAGTGCAGTGGTGCATC 570
Db 313 TTTTCTTTTATGACAGAGTCTCACTCTGTGACCCAGGCTGCAGTGCAGTGGCATGATC 254
QY 571 TCAGCTTACTGCAACTCTGCTGCGAGTTCAAGCGATTCTCATGCTCCACCTCCCAA 630
Db 253 TCAGTCTACTGAGCTCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 194
QY 631 GTAGTGGAGTACAGGATGACCAATGCCCAACTAATTTTGTATTTTATTTAGTAGAG 690
Db 193 GTAGTGGAGTACAGGACGACCACTATGCCAGCTAATTTTGTATTTTATTTAGTAGAG 134
QY 691 ACGGGTCTTTCATGTTGCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 750
Db 133 ACGAGTCTCAGCTGTTGGCAGGTTGACTCAAACTCTGACCTCAATGATGCTGCT 74
QY 751 GCCTCGGCTCCCAAGTGTATGATTACAGCGGTGACCCACCGTGCCTGCCCTAAACAT 810
Db 73 GCCTCAGCTCCCAAGTGTGAGATTACAGCGGTGACCCACCGTGCCTGCCCTAACTG 14
QY 811 TTATCTTTCTTT 823
Db 13 CTGTTTTCATGT 1
RESULT 7
US-09-269-939A-19/c
; Sequence 19, Application US/09269939A
; Patent No. 6635431
; GENERAL INFORMATION:
; APPLICANT: Bihaun, Bernard
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Yen-Potin, Frances
; TITLE OF INVENTION: LSR Receptor, Its Activity, Its Cloning and Its Application To
; TITLE OF INVENTION: The Diagnosis Prevention And/or Treatment of Obesity and
; TITLE OF INVENTION: Related Risks or Complications
; FILE REFERENCE: GENSET.035APC

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; CURRENT APPLICATION NUMBER: US/09/269,939A
; CURRENT FILING DATE: 1999-08-28
; PRIOR APPLICATION NUMBER: FR 97/10088
; PRIOR FILING DATE: 1997-08-06
; PRIOR APPLICATION NUMBER: FR 98/05032
; PRIOR FILING DATE: 1998-04-22
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patent.pm
; SEQ ID NO 19
; LENGTH: 22976
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1898..2253
; NAME/KEY: exon
; LOCATION: 3437..3781
; NAME/KEY: exon
; LOCATION: 12065..12184
; NAME/KEY: exon
; LOCATION: 15045..15101
; NAME/KEY: exon
; LOCATION: 15666..15812
; NAME/KEY: exon
; LOCATION: 19479..19652
; NAME/KEY: exon
; LOCATION: 19799..19858
; NAME/KEY: exon
; LOCATION: 19956..20087
; NAME/KEY: exon
; LOCATION: 20229..20854
; NAME/KEY: exon
; LOCATION: 20944..21094
; NAME/KEY: Misc Feature
; LOCATION: 19956..19958
; OTHER INFORMATION: Potential variant splicing site AAG
US-09-269-939A-19

Query Match      19.7%; Score 232.4; DB 4; Length 22976;
Best Local Similarity 72.9%; Pred. No. 2.8e-55;
Matches 299; Conservative 0; Mismatches 111; Indels 0; Gaps 0;

Qy 504 TTTATTTTATTCTCTTTTACACAGAGTCTCACTCTGTACACCGAGGTTCAGCGATTCTCATGCCTCCAC 623
Db 5787 TTTTTTTTTTTTTTTTTGACACAGAGTCTCACTCTGTGCGCCAGACTGCAGTACAGTGG 563
Qy 564 TGCCATCTCAGCTTACTGCACCTCTGCCTGCCAGGTTCAAGCGATTCTCATGCCTCCAC 623
Db 5727 TGCGATCTCAGCTCACTGCACCTCTGCCTCTCGGTTTCAGCCGATTCTCATGCCTCAGC 568
Qy 624 CTCCCAAGTAGCTGGGACTACAGCGATGCACCAATGCCCAACTAAATTTTGTATTTT 683
Db 5667 CTCCTGAGTAGCTGGGATTACAGGCATGTGCCACATGCCTGGCTAATCTTTGTATTTT 5608
Qy 684 AGTAGACACGGGTTTGGCCATGTTGCCAGCTGGCCTTGAAGCTCCTGSCCTCAACAA 743
Db 5607 AGTAGACACGGGTTTCCACATGTTGCCAGCTGGTCTGGAACTCTCTGACCTCAGGTGA 5548
Qy 744 TCACCTTGGCCTCGGCCCTCCCAAGTGTATGATTACAGGGGTGAGCCACCGTGCCTGGCC 803
Db 5547 TCCACCCACCTTGGCCTCCCAAGGTGTGAGATTACAGAGCTGAGCCACCGTGCCAGAC 5488
Qy 804 TAAACATTTATCTTTCTTTGTGTGGAACTTTGAAATTTATACAATGAATATTGTTAA 863
Db 5487 TTTGAAATTTCTCATACTCTTTCTTTATCTGCTTATTTTACTGCCAGTCTCACTCCACCAGA 5428
Qy 864 CTGTCACTCTCCTCTGCTGCTATGGAACACTGGGACTCTTCTCCCTCTATC 913
Db 5427 ATGTCACTCTCTTGACGACAGAAACTTCAGCCCATCCCAATCACCTCTATC 5378

RESULT 8
US-09-499-522-1/c

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RESULT 8

RESULTS
US-09-499-522-1/c

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; LOCATION: 22324..23187
; OTHER INFORMATION: homolog with USF2 gene in ref: embl Y07661
; FEATURE:

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Db 5711 AGTAGAGAGGGGTTTCCACGATGTGGCCAGGCTGTGTGGAACTCCTGACCTCAGGTGA 5652
Qy 744 TCCACTTGCCTCGGCTCCCAAGTGTATGATTACAGGCGTGAGCCACCGTGCCTGGCC 803
Db 5651 TCCACCACCTTGGCTCCCAAGTGTGTGAGATTACAGAGCTGAGCCACCGTGCCTGGCC 5592
Qy 804 TAAACATTTATCTTTTCTTGTGTGGAACTTGAATATACATGATTAATTTGTTAA 863
Db 5591 TTTGAAATTTCTACACTCTTTCTTTATCTGCTTTATTTACTGCGAGTCTCACTCCACCAGA 5532
Qy 864 CTGTCATCTCCCTGCTGTGTATGGAACACTGGGACTTCTTCCCTCTATC 913
Db 5531 ATGTCACTCTCTTGAGCAGACAAACTTCAGCCATCCCAATCACCTCTATC 5482

RESULT 9

US-09-798-096-10/c

; Sequence 10, Application US/09798096

; Patent No. 6393378

; GENERAL INFORMATION:

; APPLICANT: Donna T. Ward

; APPLICANT: Andrew T. Watt

; TITLE OF INVENTION: ANTISENSE MODULATION OF RECQL2 EXPRESSION

; FILE REFERENCE: RIS-0207

; CURRENT APPLICATION NUMBER: US/09/798,096

; CURRENT FILING DATE: 2001-03-01

; NUMBER OF SEQ ID NOS: 89

; SEQ ID NO 10

; LENGTH: 99500

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

US-09-798-096-10

Query Match 19.6%; Score 231.2; DB 4; Length 99500;
Best Local Similarity 78.1%; Pred. No. 1.4e-54;
Matches 278; Conservative 0; Mismatches 78; Indels 0; Gaps 0;
Qy 504 TTTATTTTATCTTTTTHAGACAGAGTCTCACTCTGTCCACCGAGCTGAGTGCAGTGG 563
Db 66170 TTTGTTTTTGTGTTTTTGAGACAGAGTCTCACTCTGTCCGCCAGCGTGGAGTGCAGTGG 66111
Qy 564 TGCCATCTCAGCTTACTGCAACCTCTGCCTGCCAGGTTCAAGGATTTCTCATGCCCTCCAC 623
Db 66110 CACAATCTTGGCTCACTACAACTCTGCTGCTGGGTTTCAAGCCATCTCTCTGCTCAGC 66051
Qy 624 CTCCAAAGTAGTGGGACTACAGGCAATGCAACCAATGCCCAACTAATTTTGTATTTT 683
Db 66050 CTCCAAAGTAGTGGGATTTATGATGATGCCCACTCGGCCCACTAAATTTTGTATTTT 65991
Qy 684 AGTAGACAGCGGTTTTTGCCATGTTGCCAGGCTGGCCTTGAACTCCTGGCCTCAACAA 743
Db 65990 AGTAGACAGAGTTTTCACCATGTTGCCAGGCTGGTCTCGAACTCCTGACCTCAAGCAA 65931
Qy 744 TCACTTGCCTCGGCTCCCAAGTGTATGATTACAGCGTGAGCCACCGTGCCTGGCC 803
Db 65930 TCCACTTGCCTTGGCTCCCAAGTGTGGGATTACAGGCATGAGCCACCGGCGCCAGCC 65871
Qy 804 TAAACATTTATCTTTTCTTGTGTGGAACTTGAATATACATGATTAATTTG 859
Db 65870 TACCAAGTAGTCTTAAGTTGAATTTGTGCTAGCAGCTTACACATAGACACTG 65815

RESULT 10

US-08-724-394A-20

; Sequence 20, Application US/08724394A

; Patent No. 5872237

; GENERAL INFORMATION:

; APPLICANT: Feder, John N.

; APPLICANT: Kronmal, Gregory S.

; APPLICANT: Lauer, Peter M.

; APPLICANT: Ruddy, David A.

; APPLICANT: Thomas, Winston

APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
TITLE OF INVENTION: Sequences and Antibodies Thereto
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Flits, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 017957-000100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: misc.feature
LOCATION: 1..246240
OTHER INFORMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-20

Query Match 19.5%; Score 229.2; DB 2; Length 246240;
Best Local Similarity 75.4%; Pred. No. 8.5e-54;
Matches 285; Conservative 0; Mismatches 93; Indels 0; Gaps 0;
Qy 426 TACATGTGATTTGGATACATGTATACAAATATATATGATCAATCAGGGTAACTGGGA 485
Db 85558 TAAACATGAATTCACATAATATGATACATTTATGTTTAAATTTGTGTATCTTTT 85617
Qy 486 TATCCATCACATCAAAACATTTATTTTATCTTTTAGACAGAGTCTTCACTCTGTCAAC 545
Db 85618 GGTGACTCCTTTCATTTCTTTCTTTTATTTTGTGACAGAAATCTCTCTGTCAAC 85677
Qy 546 CAGGCTGGAGTGCAGTGGTGCCATCTCAGCTTACTGCAACCTCTGCTGCCAGGTTCAAG 605
Db 85678 CAGGCTGTAGTGTAGTGGGAAATCTCAGCTCACTGCAACCTCTGCTGCCAGGTTCAAG 85737
Qy 606 CGATTCTCATGCTCCACCTCCCAAGTAGCTGGGACTACAGGCATGCAACCAATGCCCA 665
Db 85738 TGATTTCTGTCTTTCAGCTCCCAAGTAGCTGGGATTACAGGCATGTCACCAATGCCCA 85797
Qy 666 ACTAAATTTTGTATTTTATAGTAGACAGGGGTTTGGCAATGTTGCCAGGCTGGCTTCA 725
Db 85798 GCTAAATTTTGTATTTTGTGTAGAGCAGGGTTTGGCAATGTTGGGCAAGGCTGGTCTTCA 85857
Qy 726 ACTCCTGGCCTCAACAACTCCACTTCCCTCGGCCTCCCAAGTGTATGATTACAGGCT 785
Db 85858 ACTCCTGGCTTCAAGTGTATCCGCTCCCTCCCAAGTGTATGATTACAGGCT 85917
Qy 786 GAGCCACCGTGCCTGGCC 803
Db 85918 GAGCCACCACTGGCC 85935


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; PRIOR FILING DATE: 1997-08-06
; PRIOR APPLICATION NUMBER: FR 98/05032
; PRIOR FILING DATE: 1998-04-22
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patent.pm
; SEQ ID NO 41
; LENGTH: 21721
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1898..2253
; NAME/KEY: exon
; LOCATION: 3438..3782
; NAME/KEY: exon
; LOCATION: 12084..12183
; NAME/KEY: exon
; LOCATION: 15049..15105
; NAME/KEY: exon
; LOCATION: 15670..15816
; NAME/KEY: exon
; LOCATION: 19486..19659
; NAME/KEY: exon
; LOCATION: 19806..19865
; NAME/KEY: exon
; LOCATION: 19963..20094
; NAME/KEY: exon
; LOCATION: 20236..20864
; NAME/KEY: exon
; LOCATION: 20954..21094
; NAME/KEY: Misc_Feature
; LOCATION: 715
; OTHER INFORMATION: diverging nucleotide, G in ref genbank:AC002128
; NAME/KEY: Misc_Feature
; LOCATION: 1229
; OTHER INFORMATION: diverging insertion, G in ref genbank:AC002128
; NAME/KEY: Misc_Feature
; LOCATION: 3676
; OTHER INFORMATION: diverging nucleotide, T in ref genbank:AC002128
; NAME/KEY: Misc_Feature
; LOCATION: 5039
; OTHER INFORMATION: diverging deletion, G in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 5118
; OTHER INFORMATION: diverging nucleotide, C in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 7337
; OTHER INFORMATION: diverging deletion, C in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 8294
; OTHER INFORMATION: diverging nucleotide, G in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 8604
; OTHER INFORMATION: diverging nucleotide, C in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 8928
; OTHER INFORMATION: diverging nucleotide, A in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 9021
; OTHER INFORMATION: diverging nucleotide, G in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 9851
; OTHER INFORMATION: diverging insertion, GAATGAAA in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 9878
; OTHER INFORMATION: diverging nucleotide, C in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 11478
; OTHER INFORMATION: diverging nucleotide, T in ref genbank: AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 11577
; OTHER INFORMATION: diverging deletion, C in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 11779
; OTHER INFORMATION: diverging nucleotide, T in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 13411
; OTHER INFORMATION: diverging deletion, T in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 13538
; OTHER INFORMATION: diverging nucleotide, G in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 13896
; OTHER INFORMATION: diverging nucleotide, G in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 14912
; OTHER INFORMATION: diverging nucleotide, A in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 16732
; OTHER INFORMATION: diverging nucleotide, C in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 17169
; OTHER INFORMATION: diverging nucleotide, G in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 18946
; OTHER INFORMATION: diverging deletion, G in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 19474
; OTHER INFORMATION: diverging nucleotide, G in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 20500
; OTHER INFORMATION: diverging deletion, G in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 20501
; OTHER INFORMATION: diverging deletion, G in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 20502
; OTHER INFORMATION: diverging deletion, A in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 21270
; OTHER INFORMATION: diverging nucleotide, G in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 21352
; OTHER INFORMATION: diverging insertion, T in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 21476
; OTHER INFORMATION: diverging nucleotide, A in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 21588
; OTHER INFORMATION: diverging insertion, C in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 21601
; OTHER INFORMATION: diverging deletion, T in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 21635
; OTHER INFORMATION: diverging insertion, G in ref genbank:AD000684
; NAME/KEY: Misc_Feature
; LOCATION: 19963..19965
; OTHER INFORMATION: Potential variant splicing site AAG
; NAME/KEY: Misc_Feature
; LOCATION: 1..21721
; OTHER INFORMATION: n= a,g,c or t
; US-09-269-939A-41
;
; Query Match 19.4%; Score 228.2; DB 4; Length 21721;
; Best Local Similarity 82.8%; Pred. No. 4,1e-54; Indels 0; Gaps 0;
; Matches 260; Conservative 0; Mismatches 54;
;
; Qy 504 TTTATTTTATTTCTTTTGTAGACAGAGTCTCACTCTGTCCACCCAGGCTGGAGTGAGTGG 563
; Db TTTTCTTCTAGCTTACTGCAACTCTGCTGCGAGTTCACAGGATTCCTCATGCTCCAC 623
; Qy 564 TGGCATCTAGTCTACTGCAACTCTGCTGCGAGTTCACAGGATTCCTCATGCTCCAC 623
; Db 5730 TGGCATCTAGTCTACTGCAACTCTGCTGCGAGTTCACAGGATTCCTCATGCTCCAC 5671

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 16, 2004, 21:50:55 ; Search time 1923 Seconds
(without alignments)
2501.860 Million cell updates/sec

Title: US-10-063-736-130
Perfect score: 596
Sequence: 1 MGLLLVFLSLPVAAYTIM.....CVCAVHFSSHPVAVECLK 111

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-O=/cgn2_1/USPTO_spool_p/US10063736/runat_15092004_103601_10631/app.query.fasta_1.263
-DB=GenEmbl -QWTF=frastap -SUFFIX=sgs -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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6: gb.pat:*
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9: gb.pr:*
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11: gb.sts:*
12: gb.sy:*
13: gb.un:*
14: gb.vi:*
15: em.ba:*
16: em.fun:*
17: em.hum:*
18: em.in:*
19: em.mu:*
20: em.om:*
21: em.or:*
22: em.ov:*
23: em.pat:*
24: em.ph:*
25: em.pl:*
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27: em.sts:*
28: em.un:*

RESULT 1

Result No.	Score	Query Match	Length	DB	ID	Description
1	596	100.0	801	6	BD222657	Human sig
2	596	100.0	1177	6	AX922398	Sequence
3	596	100.0	1177	6	AX358958	Sequence
4	596	100.0	1177	6	AX362451	Sequence
5	596	100.0	1177	6	AX376314	Sequence
6	596	100.0	1177	6	AX454686	Sequence
7	596	100.0	1177	6	AX491164	Sequence
8	596	100.0	1177	9	AX358613	Homo sapi
9	596	100.0	3566	9	AK127751	Homo sapi
10	596	100.0	159272	9	HSDJ686C3	AK127751 Homo sapi
11	584	98.0	2560	6	AX833218	Sequence
12	584	98.0	2560	9	AK094789	Homo sapi
13	227	38.1	200521	10	AL833804	AX094789 Homo sapi
14	221	37.1	259335	2	AC130173	AL833804 Mouse DNA
15	165.5	27.8	3216	10	AF417581	AC130173 Rattus no
16	162.5	27.3	3169	9	AF417580	AF417581 Mus muscu
17	159	26.7	189755	2	BX571945	AF417580 Homo sapi
18	152.5	25.6	148762	2	BX322786	BX571945 Danio rer
19	152.5	25.6	177584	2	BX296526	BX322786 Danio rer
20	151	25.3	1977	5	AY263168	BX296526 Danio rer
21	144	24.2	2871	5	AY263167	AY263168 Takifugu
22	137	23.0	214504	10	AC102779	AY263167 Takifugu
23	137	23.0	242249	10	AC102790	AC102779 Mus muscu
24	137	23.0	340350	2	AC112299	AC102790 Mus muscu
25	136	22.8	75609	9	AL162416	AC112299 Rattus no
26	131	22.0	1528	9	AK098607	AL162416 Human DNA
27	131	22.0	2895	10	AF417579	AK098607 Homo sapi
28	131	22.0	3201	9	AF417578	AF417579 Mus muscu
29	102	17.1	208299	2	AC136865	AF417578 Homo sapi
30	102	17.1	242241	2	AC11252	AC136865 Rattus no
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32	95	15.9	124950	9	AC108059	AC006685 Caenorhab
33	94.5	15.9	1749	5	AY263172	AC108059 Homo sapi
34	94	15.8	2572	3	AY263175	AY263172 Takifugu
35	94	15.8	137009	9	AC009970	AY263175 Anopheles
36	93.5	15.7	188721	2	RM46228	AC009970 Homo sapi
37	93.5	15.7	244402	2	AC098222	AL603727 Rattus no
38	93	15.6	48836	2	AC020151	AC098222 Rattus no
39	93	15.6	164595	2	AC140976	AC020151 Drosophil
40	93	15.6	181063	3	AC010107	AC140976 Lemur cat
41	93	15.6	184657	3	AC010043	AC010107 Drosophil
42	93	15.6	285860	3	AE003551	AC010043 Drosophil
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45	92.5	15.5	179408	2	AC027234	AL157907 Homo sapi
						AC027234 Homo sapi

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

QY	Db	101 HisGlnProProValAlaValGluCysLeuIys 111	309 CACCAGCACCTGTGGCCGTGAGTGTGAA 341
RESULT 2			
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LOCUS			
DEFINITION		Sequence 129 from Patent WO0116318.	
ACCESSION		AX092398	
VERSION		AX092398.1	GI:13444513
KEYWORDS			
SOURCE			
ORGANISM			
		Homo sapiens (human)	
REFERENCE			
AUTHORS		Homo sapiens	
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
		1	
		Eaton,D.L., Filvaroff,E., Gerritsen,M.E., Goddard,A., and	
		Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Watanabe,C.K. and	
		Wood,W.I.	
		Secreted and transmembrane polypeptides and nucleic acids encoding	
		the same	
		Patent: WO 0116318-A 129 08-MAR-2001;	
		Genentech, Inc. (US)	
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ORIGIN			
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Best Local Similarity:		100.00%	Mismatches: 0
Query Match:		100.00%	Indels: 0
DB:		6	Gaps: 0
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QY	21	SerLeuProProSerPheAspCysGlyProPheArgCysArgValSerValIalaArgGlu 40	
Db	70	TCCCTCCACCCCTCTCTTTGATCGCGGCCGTTTCAGTGCAGAGCTTCAGTGCCTGGAG 129	
QY	41	HisLeuProSerArgGlySerLeuLeuArgGlyProArgProArgIleProValLeuVal 60	
Db	130	CACCTTCCTCTCCCGAGGAGCTCTGCTCAGAGGCCCTCGGCCCCAGAAATTCAGTTCTGGTT 189	
QY	61	SerCysGlnProValIysGlyHisGlyThrLeuGlyCysArgProMetProPheIysArg 80	
Db	190	TGATGCCAGCCTGTAAAAGGCCATGGAACTTGGGTGAATCACCCGATGCCATTTAAGAGG 249	
QY	81	ValPheCysGlnAspGlyAsnValArgSerPheCysValCysAlaValHisPheSerSer 100	
Db	250	GTTTCTTCGCAGATGGAAATGTTAGGTGCTTCTGTGTCTGCGCTGTTCATTTCAGTAGC 309	
QY	101	HisGlnProProValAlaValGluCysLeuIys 111	
Db	310	CACCAGCACCTGTGGCCGTGAGTGTGAA 342	

ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE	Baker,K.P., Desnovers,L., Gerritsen,M.E., Goddard,A., Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smith,V., Stephan,J.P., Watanabe,C.K. and Wood,W.I. Secreted and transmembrane polypeptides and nucleic acids encoding the same
JOURNAL	Patent: WO 0193983-A 211 13-DEC-2001;
FEATURES	Genetech Inc. (US) Location/Qualifiers source 1..1177 /db_xref="taxon:9606"
ORIGIN	/organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"
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Score:	596.00 Matches: 111
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Best Local Similarity:	100.00% Mismatches: 0
Query Match:	100.00% Indels: 0
DB:	Gaps: 0
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Dd	10 ATGGGGCTCCTGCTGTGGTCTTTCTTCAGCCCTCTCGCGGGGCCACCATCATG 69
QY	21 SerLeuProProSerPheAspCysGlyProPheArgCysArgValSerValAlaAArgGlu 40
Dd	70 TCCTCCCCACCCTCTTTGACTCGGGGCGTTACAGTGCAAGTCTCAGTTGCCCGGAG 129
QY	41 HisLeuProSerArgGlySerLeuLeuArgGlyProArgProArgIleProValLeuVal 60
Dd	130 CACCTCCCTCCCGAGGCAGCTGTCTCAGAGGGCTCGGCCCAAGAATCCAGTTCTGTGTT 189
QY	61 SerCysGlnProValIySGlyHisGlyThrLeuGlyGluSerProMetProPheLysArg 80
Dd	190 TCAATGCCAGCCTGTAAAGGCATGGAACCTTTGGTGAAATCACCGATGCCATTTAAGAGG 249
QY	81 ValPheCysGlnAspGlyAsnValArgSerPheCysValCysAlaValHisPheSerSer 100
Dd	250 GTTTTCATGCCAGATGGAATGTTAGGTGCTTCGTCTGTGCTGTTCATTTCAATTCAGTAGC 309
QY	101 HisGlnProProValAlaValGluCysLeuLys 111
Dd	310 CACCAGCACCTGTGGCCGTTGAGTGTGATAA 342
RESULT 4	
AX362451	1177 bp DNA linear PAT 15-FEB-2002
LOCUS	Sequence 211 from Patent WO0208288.
DEFINITION	
ACCESSION	AX362451
VERSION	AX362451.1 GI:18694683
KEYWORDS	
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE	Baker,K.P., Desnovers,L., Gerritsen,M.E., Goddard,A., Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smith,V., Stephan,J.P., Watanabe,C.K. and Wood,W.I. Secreted and transmembrane polypeptides and nucleic acids encoding the same
JOURNAL	Patent: WO 0208288-A 211 31-JAN-2002;
FEATURES	Genetech, Inc. (US) Location/Qualifiers source 1..1177

Qy	81	ValPheCysGlnAspGlyAsnValArgSerPheCysValCysAlaValHisPheSer	100
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Qy	101	HisGlnProProValAlaValGluCysLeuLys	111
Db	310	CACCAGCCACCTGTGGCCGTGTGAGTGCTTGAA	342
RESULT 8			
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LOCUS	AY358613	1177 bp	mRNA
DEFINITION	Homo sapiens clone DNAB1754 TWC2 (UNQ907)		linear PRI 03-OCT-2003
ACCESSION	AY358613		mRNA, complete cds.
VERSION	AY358613.1	GI:37182347	
KEYWORDS	FLI_CDNA		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J., Dowd,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B., Dend,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Haas,P.E., Haidens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S., Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C., Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V., Stinson,J., Vagts,A., Vanden,R., Watanabe,C., Wleand,D., Woods,K., Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z., Goddard,A., Wood,W.I. and Godowski,P.		
TITLE	The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment		
JOURNAL	Genome Res. 13 (10), 2265-2270 (2003)		
PUBMED	12975309		
REFERENCE	2 (bases 1 to 1177)		
AUTHORS	Clark,H.F.		
TITLE	Direct Submission		
JOURNAL	Submitted (01-AUG-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA		
FEATURES	Location/Qualifiers		
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	/translation="MGLLLVLFSLLPVAYTMSLPFSDCGPFCRVSVAREHLPS		
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ORIGIN			
Alignment Scores:			
Pred. No.:	2,41e-43	Length:	1177
Score:	596.00	Matches:	111
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0
US-10-063-736-130 (1-111) x AY358613 (1-1177)			
Qy	1	MetGlyLeuLeuLeuValLeuPheLeuSerLeuLeuProValAlaTyrThrIleMet	20
Db	10	ATGGGCTCTGTGCTGTGCTCTTCTCAGCTCTCGCGTGGCTACACCATCATG	69

SRSNNFYMGLLLVFLSLPLVAVTMSLPPSPDCGPFRCRVSAREHLPSPRGSLLRG
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 LK"

ORIGIN

Alignment Scores:
 Pred. No.: 7.33e-43 Length: 3566
 Score: 596.00 Matches: 111
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-10-063-736-130 (1-111) x AK127751 (1-3566)

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 Qy 21 SerLeuProProSerPheAspCysGlyProPheArgCysArgValSerValAlaArgGlu 40
 Db 436 TCCCTCCACCCCTCTTGTACTGCGGCGCGTTCAGGTGACAGTCTCAGTTGCCCGGAG 495
 Qy 41 HisLeuProSerArgGlySerLeuLeuArgGlyProArgProArgIleProValLeuVal 60
 Db 496 CACCTCCCTCCAGGAGCTCTCTCAGAGCGGCTCGGCCAGAAATTCAGATTCGTGTT 555
 Qy 61 SerCysGlnProValLysGlyHisGlyThrLeuGlyGluSerProMetProPheLysArg 80
 Db 556 TCATGCCAGCCCTGTAAGAGCCATGGAATTTGGTGAATCACCAGTGCATTAAGAGG 615
 Qy 81 ValPheCysGlnAspGlyAsnValArgSerPheCysValCysAlaValHisPheSerSer 100
 Db 616 GTTTCTGCCAGAGTGAATGTTAGTCTGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 675
 Qy 101 HisGlnProProValAlaValAlaCysLeuLys 111
 Db 676 CACCAGCCACCTGTGGCGGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 708

RESULT 10

HSDJ686C3/C

LOCUS

DEFINITION Human DNA sequence from clone RP4-686C3 on chromosome 20. Contains the IDH3B gene for isocitrate dehydrogenase 3 (NAD+) beta A and B, the gene for nucleolar protein NOP56, a novel gene, ESTs, STSs, GSSs and three CpG islands, complete sequence.

ACCESSION

AL049712.12 GI:5629919

VERSION HTG; CpG island; IDH3B; isocitrate dehydrogenase 3; NOP56;

KEYWORDS

nucleolar protein.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 159272)

AUTHORS

Smith, M.

TITLE

Direct Submission

JOURNAL

Submitted (09-FEB-2001) Sanger Centre, Hinxton, Cambridgeshire, requests: clonerequest@sanger.ac.uk

COMMENT

On Jul 28, 1999 this sequence version replaced gi:5578962. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em, EMBL; Sw, SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human

chromosome 20, constructed by the Sanger Centre Chromosome 20 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr20>

This sequence is the entire insert of clone RP4-686C3. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. RP4-686C3 is from the library RPCI-4 constructed by the group of Pieter de Jong. For further details see

<http://www.chori.org/bacpac/home.htm>

VECTOR: pCYPAC2.

FEATURES

Source

Location/Qualifiers

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 886..1010
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Alignment Scores:
Pred. No.: 3,34e-41 Length: 159272
Score: 596.00 Matches: 111
Percent Similarity: 100.00% Conservative: 0
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Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-063-736-130 (1-111) x HSDJ686C3 (1-159272)

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QY 21 SerLeuProProSerPheAspCysGlyProPheArgCysArgValSerValAlaArgGlu 40
Db 54672 TCCTCCACCCTCTTTGACTGCGGGCGCTTCAGGTGCAGAGTCTCAGTTGCCGGAG 54613

QY 41 HisLeuProSerArgGlySerLeuLeuArgGlyProArgProArgIleProValLeuVal 60
Db 54612 CACCTCCCTCCGAGGAGCTGTGCTCAGAGGGCCCTCGGCCAGAAATTCAGTCTCGTT 54553

QY 61 SerCysGlnProValLysGlyHisGlyThrLeuGlyGluSerProMetProPheLysArg 80
Db 54552 TCATGCCACCTGTAAAGGCATGAAATTTGGGTGAATCACCAGTGCATTAGAGG 54493

QY 81 ValPheCysGlnAspGlyAsnValArgSerPheCysValCysAlaValHisPheSerSer 100
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QY 101 HisGlnProProValAlaValGluCysLeuLys 111
Db 54432 CACCAGCACCTGTGGCCGTTGAGTCTTGAA 54400

RESULT 11
AX833218
LOCUS 2560 bp DNA linear PAT 15-DEC-2003
DEFINITION Sequence 342 from Patent EP1347046.
ACCESSION AX833218
VERSION AX833218.1 GI:39919353
KEYWORDS
SOURCE Hmo sapiens (human)
ORGANISM Hmo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Isogai,T., Sugiyana,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S.,
Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R.,
Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and
Masuko,Y.

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Full-length cDNA sequences
 JOURNAL Patent: EP 1347046-A 342 24-SEP-2003;
 Research Association for Biotechnology (JP)
 FEATURES Location/Qualifiers
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 /db_xref="taxon:9606"
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 Db 1747 GTTTTCTGCCAGATGGAATGTTAGTCTGTCTGTGCTGCGCTGTCATTTCAGTAGC 1806
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 Db 1807 CACCAGCACCTGTGGCCGTTGAGTGTGTTGAAA 1839
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 VERSION AK094789.1 GI:21753918
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 AUTHORS Suzuki,O., Sasaki,N., Aotsuka,S., Shoji,T., Ichihara,T.,
 Shiohata,N., Matsumoto,K., Hirano,M., Sano,S., Nomura,R.,
 Yoshikawa,Y., Matsumura,Y., Mouriya,S., Chiba,E., Momiyama,H.,
 Onogawa,S., Kaeriyama,S., Satoh,N., Matsumura,H., Takahashi,E.,
 Kataoka,R., Kuga,N., Kuroda,A., Satoh,I., Kanata,K., Takami,S.,
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 Watanabe,M., Murakawa,K., Kanehori,K., Takahashi-Fujii,A.,
 Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S.,
 Nagahara,K., Masuho,Y., Nagai,K. and Isogai,T.
 NEDO human cDNA sequencing project
 Unpublished
 2 (bases 1 to 2560)
 Isogai,T. and Yamamoto,J.
 Direct Submission
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 JOURNAL Patent: EP 1347046-A 342 24-SEP-2003;
 Research Association for Biotechnology (JP)
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 QY 21 SerLeuProSerPheAspGlyProPheArgCysArgValSerValAlaArgGlu 40
 Db 1567 TCCCTCCACCTCTTTGACTGCGGCCGTTTACGGTCAGAGTCTCAGTTGCCAGGAG 1626
 QY 41 HisLeuProSerArgGlySerLeuLeuArgGlyProArgProArgIleProValLeuVal 60
 Db 1627 CACCTCCCTCCGAGGAGCTGCTCAGAGGCGCTTGGCCAGAAATTCAGTTCTGGTT 1686
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 QY 101 HisGlnProProValAlaValGluCysLeuLys 111
 Db 1807 CACCAGCACCTGTGGCCGTTGAGTGTGTTGAAA 1839
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 LOCUS Mouse DNA sequence from clone RP23-20A6 on chromosome 2, complete
 DEFINITION
 ACCESSION AL833804
 VERSION AL833804.16 GI:32187965
 KEYWORDS HTG.

Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7
 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
 (E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
 NEDO human cDNA sequencing project supported by Ministry of
 Economy, Trade and Industry of Japan; cDNA full insert sequencing:
 Research Association for Biotechnology (RAB); cDNA library
 construction: Helix Research Institute (HRI) (supported by Japan
 Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
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 Evaluation; clone selection for full insert sequencing: HRI and
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 Query Match: 97.99% Indels: 0
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 QY 1 MetGlyLeuLeuLeuValLeuPheLeuSerLeuLeuProValAlaTyrThrIleMet 20
 Db 1507 ATGGGCTCTCTGCTGCTCTCTCTCAGCCTCTGCGGCTGAGCTACACCATCATG 1566
 QY 21 SerLeuProSerPheAspGlyProPheArgCysArgValSerValAlaArgGlu 40
 Db 1567 TCCCTCCACCTCTTTGACTGCGGCCGTTTACGGTCAGAGTCTCAGTTGCCAGGAG 1626
 QY 41 HisLeuProSerArgGlySerLeuLeuArgGlyProArgProArgIleProValLeuVal 60
 Db 1627 CACCTCCCTCCGAGGAGCTGCTCAGAGGCGCTTGGCCAGAAATTCAGTTCTGGTT 1686
 QY 61 SerCysGlnProValLysGlyHisGlyThrLeuGlyCysSerProMetProPheLysArg 80
 Db 1687 TCATGCCAGCTGTAAAGGCCATGGAACCTTGGTGAATCACCAGTGCATTAAGAGG 1746
 QY 81 ValPheCysGlnAspGlyAsnValArgSerPheCysValCysAlaValHisPheSerSer 100
 Db 1747 GTTTTCTGCCAGATGGAATGTTAGTCTGTCTGTGCTGCGCTGTCATTTCAGTAGC 1806
 QY 101 HisGlnProProValAlaValGluCysLeuLys 111
 Db 1807 CACCAGCACCTGTGGCCGTTGAGTGTGTTGAAA 1839
 RESULT 13
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 LOCUS Mouse DNA sequence from clone RP23-20A6 on chromosome 2, complete
 DEFINITION
 ACCESSION AL833804
 VERSION AL833804.16 GI:32187965
 KEYWORDS HTG.

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VERSION						
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SOURCE						
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REFERENCE						
AUTHORS						

ORGANISM Mus musculus
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 1 (bases 1 to 3216)
 Kurima,K., Peters,L.M., Yang,Y., Riazuddin,S., Ahmed,Z.M., Naz,S.,
 Arnaud,D., Drury,S., Mo,J., Makishima,T., Ghosh,M., Menon,P.S.N.,
 Deshmukh,D., Oddoux,C., Ostrer,H., Khan,S., Raizuddin,S.,
 Deininger,P.L., Hampton,L.L., Sullivan,S.L., Battley,J.F.,
 Keats,B.J.B., Wilcox,E.R., Friedman,T.B. and Griffith,A.J.
 Dominant and recessive deafness caused by mutations of a novel
 gene, TMCL, required for cochlear hair-cell function
 Nat. Genet. 30 (3), 277-284 (2002)
 21918583
 MEDLINE 11850618
 PUBMED 2 (bases 1 to 3216)
 REFERENCE Kurima,K., Griffith,A.J. and Friedman,T.B.
 Direct Submission
 TITLE Submitted (10-SEP-2001) NIDCD, NIH, 5 Research Court, #2A02,
 JOURNAL Rockville, MD 20850, USA
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gene

CDS

ORIGIN

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)
12053.425 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

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- 29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	238.8	20.3	533	28	AQ471624	AQ471624 CITBI-E1-
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8	235.2	20.0	962	28	AQ744089	AQ744089 HS_5501_A
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92      224.4      19.1      363      9      AL120151
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94      224.4      19.1      371      12      BG222564
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96      224.4      19.1      390      13      BU588888
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VERSION      AQ203589.1 GI:3614159
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REFERENCE      1 (bases 1 to 472)
AUTHORS      Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
TITLE      Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
JOURNAL      Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE      99380589
PUBMED      10449764
COMMENT      Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3103 Row: H Column: 20
Class: BAC ends
High quality sequence stop: 472.
Location/Qualifiers
1..472
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=3103 Col=20 Row=H"
/sex="male"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBelcBAC11; BAC Clones in
E-Coli DH10B"

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FEATURES

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source
1..472
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=3103 Col=20 Row=H"
/sex="male"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBelcBAC11; BAC Clones in
E-Coli DH10B"

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ORIGIN

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Query Match      36.6%; Score 430.6; DB 28; Length 472;
Best Local Similarity 98.9%; Pred. No. 1.6e-78;
Matches 444; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
QY      196      CAGCTGTAAAGGCGCATGGAACACCTTGGTGAATCACCAGTCCCATTTAAAGGGTTTC 255
DB      24      CGCCTGTAAAGGCGCATGGAAC- TTGGTGAATCACCAGTCCCATTTAAAGGGTTTC 82
QY      256      TGCCAGGATGGAATGTTAGTTCGTTCTGTCTGCTGCGTGTTCATTTTCAGTAGCCACCAG 315
DB      83      TGCCAGGATGGAATGTTAGTTCGTTCTGTCTGCTGCGTGTTCATTTTCAGTAGCCACCAG 142
QY      316      CCACCTGTGGCGGTGAGTGTGTTGAAATGAGAACTGAGAAATTAATTTCTCATGTATT 375
DB      143      CCACCTGTGGCGGTGAGTGTGTTGAAATGAGAACTGAGAAATTAATTTCTCATGTATT 202
QY      376      TTTTCTCATTTATTATTATTTTAACTGATAGTTGTACATATTGGGGGTACATGTGAT 435
DB      203      TTTTCTCATTTATTATTATTTTAACTGATAGTTGTACATATTGGGGGTACATGTGAT 262
QY      436      ATTGGATACATGTATACAAATATATATATGATCAAAATCAGGTAACTGGGATATCCATCAC 495
DB      263      ATTGGATACATGTATACAAATATATATATGATCAAAATCAGGTAACTGGGATATCCATCAC 322
QY      496      ATCAACATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 555
DB      323      ATCAACATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 382
QY      556      TGCAGTGTGGCATCTCAGCTTACTGCAACCTTGCCTGCCAGGTTCAGCGATTCTCAT 615
DB      383      TGCAGTGTGGCATCTCAGCTTACTGCAACCTTGCCTGCCAGGTTCAGCGATTCTCAT 442
QY      616      GCCTCCACCTCCCAAGTAGCTGGGACTAC 644
DB      443      GCCTCCACCTCCCAAGTAGCTGGGACTAC 471

RESULT 2
AQ139929      376 bp      DNA      linear      GSS 24-SEP-1998
LOCUS      HS_3104_A2_D10_MF CIT Approved Human Genomic Sperm Library D Homo
DEFINITION      sapiens genomic clone Plate=3104 Col=20 Row=G, genomic survey
sequence.
ACCESSION      AQ139929
VERSION      AQ139929.1 GI:3530582
KEYWORDS      GSS.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 376)
AUTHORS      Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
TITLE      Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
JOURNAL      Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE      99380589
PUBMED      10449764
COMMENT      Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3104 Row: G Column: 20
Class: BAC ends
High quality sequence stop: 376.
Location/Qualifiers
1..376
/organism="Homo sapiens"

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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="plate=3104 Col=20 Row=G"
/sex="male"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/notes="Organ: sperm; Vector: pBelBAC11; BAC Clones in
E-Coli DH10B"

ORIGIN
Query Match 30.0%; Score 353.6; DB 28; Length 376;
Best Local Similarity 96.3%; Pred. No. 1.2e-62;
Matches 362; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
QY 263 ATGGAATGTTAGGTCGTTCTGTCGCTGCTGTTTCATTTAGTACGACGACGACCTG 322
Db 1 ATGGAATGTTAGGTCGTTCTGTCGCTGCTGTTTCATTTAGTACGACGACGACCTG 60
QY 323 TGGCGTTGAGTCGTTGAAATGAGAACTGAGAAATTAATTTTCATGTAATTTTCTCA 382
Db 61 TGGCGTTGAGTCGTTGAAATGAGAACTGAGAAATTAATTTTCATGTAATTTTCTCA 120
QY 383 TTATTTATTAATTTTAACTGATAGTTGTACATATTTGGGGTACATGTCATTTTGA 442
Db 121 TTATTTATTAATTTTAACTGATAGTTGTACATATTTGGGGTACATGTCATTTGA 180
QY 443 TACATGTATACATATATAATGATCAAAATCAGGTAATCGGATATCAATCAATCAAAAC 502
Db 181 TACATGTATACATATATAATGATCAAAATCAGGTAATCGGATATCAATCAATCAAAAC 240
QY 503 ATTTATTTTATTTCTTTTATGACAGAGTCACCTCTGTCACCCAGGCTGAGTGCAGTG 562
Db 241 ATTTATTTTATTTCTTTTATGACAGAGTCACCTCTGTCACCCAGGCTGAGTGCAGTG 300
QY 563 GTGCCATCTACGTTACTGCAACCTCTGCTGCCAGGTTCAAGGATTTCTCATGCTTCCA 622
Db 301 GTGCCATCTACGTTACTGCAACCTCTGCTGCCAGGTTCAAGGATTTCTCATGCTTCCA 360
QY 623 CTCTCCAGTAGCTGG 638
Db 361 TCTCTCAAGATTTCTTG 376

RESULT 3
BM565530
LOCUS in2ed08.x1 Human insulinoma Homo sapiens cDNA 3', mRNA sequence.
DEFINITION BM565530
ACCESSION BM565530.1 GI:18825776
VERSION EST.
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 653)
Lemishka,J., Scarce,J., Kelly,G., Permutt,A., Lee,C., Kaestner,K.,
Melton,D., Brown,J., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Elistain,A.,
Schmitt,A., Theising,B., Ritter,E., Ronko,T., Bennett,J.,
Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagarisvili,R.,
Williams,T., Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. J. Ferrer In vivo mass-excised to
pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington
University Genome Sequencing Center For information on obtaining a

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clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
Seq primer: -40UP from Gibco
High quality sequence stop: 476.
Location/Qualifiers
source
1. 653
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="Insulinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="Human insulinoma"
/notes="Organ: pancreas; Vector: pBluescript SK-; Site 1:
XhoI; Site 2: EcoRI; Constructed with lambda ZAPII system
(Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
pBluescript SK- by Dr. H. Inoue following the Washington
University protocol
(http://genome.wustl.edu/est/lambda_protocol.shtml).
Please contact Hiroshi Inoue, MD/PhD for further
information on this library (Metabolism Division, Permutt
Laboratory, Washington University School of Medicine, Box
8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this
is a Washington University Pancreas EST project library."

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ORIGIN

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Query Match 25.9%; Score 305; DB 12; Length 653;
Best Local Similarity 73.4%; Pred. No. 1.2e-52;
Matches 481; Conservative 0; Mismatches 145; Indels 29; Gaps 6;
QY 508 TTTTATTTCTTTTATGACAGAGTCTCAGTC-TGTCACCCAGGCTGGAGTGAGTGCGTGC 566
Db 2 TTTTATTTTCTTTTATGACAGAGTTCAGTCTTTGTTGCCAGGCTGGAGTGAATGGCGT 61
QY 567 CATCTCAGCTTACTGCAACCTCTGCTGCCAGGCTTCAAGCGATTTCTCATGCTCCACCTC 626
Db 62 GATCTCGGCTCACCACAACTCTGCTCCAGGTTCAACAAATTC---TGCCTCAGCCTC 118
QY 627 CCAAGTAGCTGGAGCTACAGGATGACCAATGCCCAACTAAATTTTGTATTTTGT 686
Db 119 CCAAGTAGCTGGAGTACAGGATGACCAACACCGCTGGCTAATTTT---GTTTGTAGT 174
QY 687 AGAGACGGGTTTGGCCATGTTGCCAGGCTGGCTTGAACCTCCCTGGCTGCAACATCC 746
Db 175 AGAGACAGGTTTCTCAATGTTGTCAGGCTGGCTTCAAACTCCGACCTCAGGTGATCC 234
QY 747 ACTTGCTCGGCTCCCAAAGTGTATGATTACAGCGTGAGCCACCGTGCCTGCCT-- 804
Db 235 GCCACCTTGGCTCCCAAAGTGTGGATACAGGATGAGCCACCGCCACCTG 294
QY 805 -----AAACATTTATCTTTTCTTTGTTGGGAACCTTGAATATATAC 847
Db 295 TCTTTTCTTTATGCTAGAAATATTCAAATTACATTCAGTTATTTTGAATAATATATAC 354
QY 848 AATGAATATTGTTAACTGTCATCTCCCTGCTGTGTGTAAGAACACTGGAGCTTCTTCC 907
Db 355 AACAGATTATTGFAAACTACTAGTCACTTACTGATCTAGCAACAAATGGTGCTAC-TGCT 413
QY 908 TCTATCTAATGTAATTTGTACAGGTAAACCAACCGTACTTTCATCCCGACCTCTCTCTA 967
Db 414 TCTATCAAACTGTATATTTGTAACATTAATTAACCAACCTCTCTCTCTCTCTCTCTA 473
QY 968 TCCTTCCCAACCTCTGATCACC-TCAATCTACTCTCTACCTCCATGAGATCCACATTTT 1026
Db 474 CTTTCTCTAGTCTCTGGTTACCAACAACTACTCTTTATCTTTATGAGATCCCAATTTT 533
QY 1027 AGCTCCCACTGTAGTAAAGAAATGCAATATTTGCTTTTCTGCTGCTGGCTTATTTTCA 1086
Db 534 ATCTACTATATAAGTGAGAACTGTGATATTTGCTTTCTGTACTTGGCTTATTTTCA 593
QY 1087 TTAACATATGACTCTCTGTTCCATCCAGTGTGCTGCAATGACAGGATTTCTGTT 1141
Db 594 TTAACATATGACTCTCTGTTCCATCCAGTGTGCTGCAATGACAGGATTTCTGTT 648

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RESULT 4
BX382054      1201 bp      mRNA      linear      EST 08-MAY-2003
LOCUS      BX382054 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION      clone CSODI073YL08 5-PRIME, mRNA sequence.
ACCESSION      BX382054
VERSION      BX382054.1 GI:30455012
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 1201)
AUTHORS      Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE      Full-length cDNA libraries and normalization
JOURNAL      Unpublished (2001)
COMMENT      Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 559.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODI073DF04QPI&cluster=559.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODI073DF04QPI.
FEATURES
    source
    1..1201
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="CSODI073YL08"
    /tissue_type="PLACENTA COT 25-NORMALIZED"
    /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
    /note="1st strand cDNA was primed with a NotI-oligo(dT)
    primer. Five prime end enriched, double-strand cDNA was
    digested with Not I and cloned into the Not I and EcoR V
    sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
Query Match      20.7%; Score 244; DB 13; Length 1201;
Best Local Similarity 67.8%; Pred. No. 4.4e-40;
Matches 431; Conservative 0; Mismatches 170; Indels 35; Gaps 5;

QY 523 AGACAGAGTCTCAGTCTCTGCTACCCAGGCTGGAGTGGTGCATCTCAGCTTACTGC 582
DB |||||
QY 583 AACCTTCGCTGCCAGGTTCAAGGATTCCTCATGCTCCACCTCCCAAGTAGCTGGACT 642
DB |||||
QY 513 AACCTTCGCTCCCGGATTCAGCAATTCCTCTCCACAGCTCTCTAAGTAGCTAGGACT 572
DB |||||
QY 643 ACAGCGATGCCACCAATGCCCACTAATTTTGTATTTTAGTAGAGACGGGTTTTC 702
DB |||||
QY 573 ACACGATGCCACCAACCTGGCTAATTTTGTATTTTAGTAGGACGGGTTTTCAC 632
DB |||||
QY 703 CATGTTGCCAGGCTGGCTTGAATCTCTGCGCTCAACCAATCACTTGGCTGGCGCTCC 762
DB |||||
QY 633 CTGGTTGGCCAGGCTGGTCTCGAATCTCTGACCTCATGTGATCGCTCCACTTCAGCGTCC 692
DB |||||
QY 763 CAAAGTGTATGATTACAGGCGTGAGCCAGCTGGCTGGCTTAACATTTATCTTTCTT 822
DB |||||
QY 693 CAAAGTGTGGGATTACAGGATGAGCCAGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 734
DB |||||
QY 823 TGTGTTGGGAATTTGAAATATATACAAATGAATTTTGTATTTACTGTCTATCTCCCTGTG 882
DB |||||
QY 735 --CTTTTAGTATTTTAAATGTACAAATAATTTGTTGTTGTTGTTGTTGTTGTTGTTG 792
DB |||||
QY 883 CTATGGAACACTGGGACTTCTCCCTCTATCTACTGTATTTTGTACCTAGTTAACCAAC 942
DB |||||
QY 793 CTATAAATACGAATCTTATACATCTTAGCTATATTTTATATCTCATTAATCATCTCTCC 852
DB |||||

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QY 943 CGTACTTATCCCACTCCTCTCTATCTCTCCCAACCTCTGATCACCTCATTTCTACTCTC 1002
DB |||||
QY 853 TT-----TCCCACTTCAACTACCTCTTAGCTCTGTTAGCATCGTTCTGGTAT 905
DB |||||
QY 1003 TACCTCCATGAGATCCACT-----TTTTAGTCCCAATGATGATGATGATGATGATGAT 1058
DB |||||
QY 906 CACCATGAGTTTATTTGTTTTCATTTTTCATTTTTCATTTTTCATTTTTCATTTTTCATTT 965
DB |||||
QY 1059 TTGCTTTTCTGCTGCTGCTTATTTCACTTAACATTAATGACTTCTGTTCCATCATGTT 1118
DB |||||
QY 966 TTGCTTTTCTGCTGCTGCTTTCATTTTTCATTTTTCATTTTTCATTTTTCATTTTTCATTT 1021
DB |||||
QY 1119 GCTCAATGACAGGATTTGCTTTCTTATTTTCAATT 1154
DB |||||
QY 1022 GTTGAAGTACAGCATCTCATTTTTCATTTTTCATTTTTCATTTTTCATTTTTCATTTTTCATTT 1057
DB |||||

RESULT 5
AG128163      655 bp      DNA      linear      GSS 04-NOV-2001
LOCUS      Pan troglodytes DNA, clone: PTB-139D22.F, genomic survey sequence.
DEFINITION      AG128163
ACCESSION      AG128163
VERSION      AG128163.1 GI:16657328
KEYWORDS      GSS.
SOURCE      Pan troglodytes (chimpanzee)
ORGANISM      Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE      1
AUTHORS      Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
            Totoki, Y., Watanabe, H. and Sakaki, Y.
TITLE      BAC end sequences of Library PTB
JOURNAL      Unpublished
REFERENCE      2 (bases 1 to 655)
AUTHORS      Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
            Totoki, Y., Watanabe, H. and Sakaki, Y.
TITLE      Direct Submission
JOURNAL      Submitted (02-AUG-2001) Asso Fujiyama, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Japan
            1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            (E-mail: chimbes@sc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/,
            Tel: 81-45-503-9111, Fax: 81-45-503-9170)
COMMENT      Clones are derived from the chimpanzee BAC library PTB This BAC end
            was generated during the Rad process and may have higher chance of
            clone tracking errors.
PRIMERS
Sequencing: -21M13
LIBRARY
Vector      : pKS145
R.Site 1    : SacI
R.Site 2    : SacI.
FEATURES
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    /organism="Pan troglodytes"
    /mol_type="genomic DNA"
    /db_xref="taxon:9598"
    /clone="PTB-139D22.F"
    /sex="male"
    /cell_type="lymphoblast"
    /clone_lib="PTB Chimpanzee Male BAC Library"
ORIGIN
Query Match      20.5%; Score 241.6; DB 29; Length 655;
Best Local Similarity 69.3%; Pred. No. 1.5e-39;
Matches 413; Conservative 0; Mismatches 154; Indels 29; Gaps 5;

QY 573 AGCTTACTCCAACTCTGCTGCCAGGTTCAAGCATTTCTATGCTCCACTCCCAAGT 632
DB |||||
QY 78 AGCTCACTCAGCTTCAACTCTCTGGTTTCAGCAGTCTCCCGCTCAGCTCCCAAGT 137
DB |||||
QY 633 AGCTGGACTACAGGATGCACCAATGCCCAACTAA-TTTTGTATTTTAGTAGAGA 691
DB |||||

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FEATURES             Location/Qualifiers
  source              1..649
                    /organism="Pan troglodytes"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:9598"
                    /clone="PTB-054A11.F"
                    /sex="male"
                    /cell_type="lymphoblast"
                    /clone_lib="PTB Chimpanzee Male BAC Library"

ORIGIN
Query Match          20.0%; Score 235.8; DB 29; Length 649;
Best Local Similarity 78.6%; Pred. No. 2.3e-38;
Matches 282; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

QY 503 ATTATTTTATTTCTTTTGGAGAGAGTCTCAGTCTGTCACCCAGGCTGGAGTGAGTG 562
DB 547 ATTTTATTTTATTTTGGAGAGAGTCTCAGTCTGTCACCCAGGCTGGAGTGAGTG 488

QY 563 GTGCCATCTCAGCTTACTGCAACCTCTGCTGCCAGGTTCAAGCGATTCATGCTCCCA 622
DB 487 GTGTAATTTTGGCTCAGTCTGCAACCTCTCAGGTTCAAGCAATTCCTGCTCAA 428

QY 623 CTCTCCAGTAGCTGGAGTACAGGATGACCAATGACCAATGACCAATGACCAATGAC 682
DB 427 CTCTCCAGTAGCTGGAGTACAGGATGACCAATGACCAATGACCAATGACCAATGAC 368

QY 683 TAGTAGAGAGGGGTTTGTGCTGTCAGGAGTGGCTGTCAGGAGTGGCTGTCAGGAG 742
DB 367 TAGTAGAGAGGGGTTTGTGCTGTCAGGAGTGGCTGTCAGGAGTGGCTGTCAGGAG 308

QY 743 ATCCATTTGCTCGGCTCCCAAGTGTATGATACAGGAGTGGAGCCAGTGGCTGGC 802
DB 307 ATCTGCCGCTGCTCGGCTCCCAAGTGTATGATACAGGAGTGGAGCCAGTGGCTGGC 248

QY 803 CTAAACATTTATCTTTTCTGTTGGAACTTTGAAATATACAAATGATGATGATTT 861
DB 247 CGAATATCTGATTTTATGTCACAAAGTATGATGATGATGATGATGATGATTT 189

RESULT 8
AQ744089/c          962 bp DNA linear GSS 16-JUL-1999
LOCUS              HS_5501_A2_G02_T7A_RPCI-11 Human Male BAC Library Homo sapiens
DEFINITION          genomic_clone Plate:1077 Col=4 Row=M, genomic survey sequence.
ACCESSION           AQ744089
VERSION             AQ744089.1 GI:5521611
KEYWORDS            GSS.
SOURCE              Homo sapiens (human)
ORGANISM            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 962)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380599
10449764
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:

FEATURES             Location/Qualifiers
  source              1..962
                    /organism="Homo sapiens"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:9606"
                    /clone="Plate=1077 Col=4 Row=M"
                    /sex="male"
                    /clone_lib="RPCI-11 Human Male BAC Library"
                    /note="vector: pBACE3.6; Site 1: EcoRI; Site 2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
EcoRI Methylase. Size selected DNA was cloned into the
pBACE3.6 vector at EcoRI sites"

ORIGIN
Query Match          20.0%; Score 235.2; DB 28; Length 962;
Best Local Similarity 67.6%; Pred. No. 2.9e-38;
Matches 330; Conservative 0; Mismatches 158; Indels 0; Gaps 0;

QY 332 AGTGCTTGAATGAGAACTGAGAAATTAATTTCTCATGTATTTTCTCATTTATTTAT 391
DB 744 AGAGCTGAGAGAGCCAGGTTATATGAGTGAACAACCTCATTTTCTGCTGTGAAT 685

QY 392 TAAATTTTAACTGATAGTTGTACATATTTGGGGGTACATGTGATTTGGATCATGAT 451
DB 684 AAAATAACAATGGCTATGCTAGAACCGTAGTGAATAATGTAATAACACCTGTAA 625

QY 452 ACAATATATATGATCAATCAGGTACTGGATATCCATCACATCAACATTTATTTT 511
DB 624 ACTGAAAGTACTATATGAGGAGAGGATAGTTTATGAACACAAAGCATTTT 565

QY 512 TTATTTCTTTTAGACAGAGTCTCAGTCTGTCCAGGCTGGAGTGGAGTGGCTGCT 571
DB 564 TTTTCTTTTAGACAGAGTCTCAGTCTGTCCAGGCTGGAGTGGAGTGGCTGCT 505

QY 572 CAGCTTACTGCAACTCTGCTGCCAGGTTCAAGGATTTCTATGCTCCACCTCCCAAG 631
DB 504 TGGCTCAGTGCACCTCTGCTGCTGTTCAAGCAATTTCTGTGCCACACCTCCCAAG 445

QY 632 TAGCTGGAGTACAGGATGACCAATGCCCACAACTAAATTTTGTATTTTAGTAGAGA 691
DB 444 TAACTGGGATTTACAGGATGAGCCACCGTATCCAGTAATTTTGTGTTTAGTAGAGA 385

QY 692 CGGGGTTTGGCATTTGCCAGGCTGCCCTTGAATCTCTGCGCTCAAAACATCCACTTG 751
DB 384 TGGGGTTTCTCCATGCTGCCAGGCTGTTGAATCTCTGCGCTCAAAAGTATCCACCA 325

QY 752 CTCTGGCTCCCAAGTGTATGATTACAGGCTGAGCCACCGTGGCTGGCTAAACATT 811
DB 324 CTCTGGCTCCCAAGTGTCTGGATGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCA 265

QY 812 TATCTTTT 819
DB 264 TACTTTT 257

RESULT 9
BX419685/c         951 bp mRNA linear EST 13-MAY-2003
LOCUS              BX419685 Homo sapiens FETAL BRAIN Homo sapiens cdna clone
DEFINITION          CS0DF019YF13 5-PRIME, mRNA sequence.
ACCESSION           BX419685
VERSION             BX419685.1 GI:30642533
KEYWORDS            EST.
SOURCE              Homo sapiens (human)
ORGANISM            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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REFERENCE      1 (bases 1 to 951)
AUTHORS       Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE         Full-length cDNA libraries and normalization
JOURNAL       Unpublished (2001)
COMMENT       Contact: Genoscope
               Genoscope - Centre National de Sequencage
               BP 191 91006 EVRY cedex - France
               Email: seqrefgenoscope.cns.fr, Web : www.genoscope.cns.fr
               Library was constructed by Life Technologies, a division of
               Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL :
               http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
               Faraday Avenue Genoscope sequence ID : CS0DF019CC07Qp1.

FEATURES             Location/Qualifiers
     source            1..951
                        /organism="Homo sapiens"
                        /mol_type="mRNA"
                        /db_xref="taxon:9606"
                        /clone="CS0DF019YF13"
                        /tissue_type="FETAL BRAIN"
                        /dev_stage="fetal"
                        /clone_lib="Homo sapiens FETAL BRAIN"
                        /note="Torgan; brain; Vector: pCMVSPORT_6; 1st strand cDNA
                        enriched, double-strand cDNA was digested with Not I and
                        cloned into the Not I and EcoRV sites of the pCMVSPORT 6
                        vector. Library was not normalized."

ORIGIN
Query Match          19.9%; Score 234.6; DB 13; Length 951;
Best Local Similarity 80.2%; Pred. NO. 3.9e-38;
Matches 267; Conservative 6; Mismatches 60; Indels 0; Gaps 0

QY    495 CATCAACATTTATTATTTTTTATCTTTTAGACAGACTCTCACTCTGTACCAGGCTCGA 554
      : :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db     881 MACMWCVCYTITTTTTTTTTTTTTTTTGAGACGGAGTCTCACTCTGTACCAGGCTGA 822

QY    555 GTGCAGTGTGTCATCTCAGCTTACTGCAACTCTGCTGCCAGTTCAAGCGAATCTCA 614
      : :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db     821 GTGCAGTGTGCAATCTCAGCTCACTGCAATCTCTGCTTCTGGATTCAAGCAATCTTG 762

QY    615 TGCCCTCCACTCCCAGTAGCTGGGACTACAGGCATCACCAATGCCCACTAAATTTT 674
      : :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db     761 TGCCTCAGCCTCCCAAGTAGCTGGGATWACAGGTGCGCCATCATACCCAGTTAATTTT 702

QY    675 TGTATTTTGTAGACAGCGGGTTTGCCATGTGCCAGGCTGGCCTTGAACCTCTCGC 734
      : :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db     701 TGTATTTTGTAGACAGTGGGCTTTGTCATGTGCGCAGGCTGGTCTTGAACCTCTGAC 642

QY    735 CTCACAACATCACTTGCTCGGCTCCCAAGGTGTATGATTACAGGCGTGAGCCACG 794
      : :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db     641 CTCAAATGATCGCTTGCTTGGCTCCCAAGGTGCGGATAACAGGCGTGAGCCACTG 582

QY    795 TGCCCTGGCTAAACATTTATCTTTTCTTTGT 827
      : :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db     581 TGCCCGGCTCACAGGCTACTTTTCTTTTCT 549


RESULT 10
BC025670 LOCUS
DEFINITION Homo sapiens, clone IMAGE:5202535, mRNA.
ACCESSION BC025670
VERSION BC025670.1 GI:22213024
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2040)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (06-MAR-2002) National Institutes of Health, Mammalian
           Gene Collection (MGC), Cancer Genomics Office, National Cancer

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Db      84  CATTCTTTTATTTTATTTTGTGACAGAGTCTCGCTCTGTGCCGAGACTGGAGTGCAGT 143
QY      562  GTGGCACTCTAGCTTACTGCAACCTCTGCTGCCAGGTTCAAGCGATTCTCATGCTCTCC 621
Db      144  GGTGGAGTCTTGGCTGACTGCAACCTCTGCTTCTGGGTTCAAGCGATTCTCTGCTCTCG 203
QY      622  ACCTCCCAAGTAGCTGGGACTACAGGATGACACCAATGCCCACAACTAAATTTTGTATTT 681
Db      204  GCTTCCCGAGTAGCTGGGATTACAGACGTGGCGCACCATGCGCGCTAAATTTTGTATTT 263
QY      692  TTATAGAGAGCGGGTTTTTGGCATGTTGCCAGGCTGGCCTTGAACCTCTGGCTCAAAAC 741
Db      264  TTATGAAACAGGGTTTTTGGCATGTTGGCCAGGCTGGTCTTGAACCTCTGGCTCAATT 323
QY      742  ATCCACTTGGCTCGGCTCTCCAAAGTGTATGATTACAGCGGTGAGCCACCGTGCCTGG 801
Db      324  GATCCACTGCTGCTGGCTCTCCAAAGTGTGGGATTACAGGCATGAGCCACTGCACCCAG 383
QY      802  CCTAA 806
Db      384  CCTAA 388

RESULT 13
BX480642
LOCUS      633 bp mRNA linear EST 04-SEP-2003
DEFINITION DXFZp686124222_r1.686 (synonym: hlcc3) Homo sapiens CDNA clone
ACCESSION  DXFZp686124222.5, mRNA sequence.
VERSION     BX480642
KEYWORDS    EST.
SOURCE      BX480642.1 GI:31917552
ORGANISM    Homo sapiens (human)
REFERENCE   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS     Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE       1 (bases 1 to 633)
JOURNAL     Bahr, A., Lauber, J., Mewes, H.W., Weil, B., Amid, C., Osanger, A.,
COMMENT     EST (Bahr, A., Lauber, J., Mewes, H.W., Weil, B., et al.)
            Unpublished (2003)
            Contact: MIPS
            MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
            This is the 5' sequence of the clone insert
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
            sequenced by Qiagen (Hilden/Germany) within the CDNA sequencing
            consortium of the German Genome Project.
            No sl sequence available.
            This clone (DKFZp686124222) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin- Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES   Location/Qualifiers
            source          1..633
                        /organism="Homo sapiens"
                        /mol_type="mRNA"
                        /db_xref="taxon:9606"
                        /clone="DKFZp686124222"
                        /dev_stage="adult"
                        /lab_host="DH10B"
                        /clone_lib="686 (synonym: hlcc3)"
                        /note="vector: pTriplex2; Site_1: SfiIA; Site_2: SfiIB;
                        CDNA-collection"
ORIGIN
Query Match      19.6%; Score 230.6; DB 13; Length 633;
Best Local Similarity 81.8%; Pred. No. 2.7e-37;
Matches 266; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY      504  TTATTTTATTTTATTTTATGACAGAGTCTCACTCTGTACCCAGGCTGGAGTGCAGTGG 563
Db      37   TTTTATTTTATTTTATTTTATGAGTGGAGTCTCGCTCTGTACCCAGGCGGAGTGCAGTGG 96

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QY      564  TGCCATCTCAGCTTACTGCAACCTCTGCTGCCAGGTTCAAGCGATTCTCATGCTCTCCAC 623
Db      97   TGCATCTCAGCTCACTGCAACCTCTGCTCTGCTCTGCTTCAACGATTCTCTGCTCAGC 156
QY      624  CTCCCAAGTAGCTGGGACTACAGGATGACACCAATGCCCACAACTAAATTTTGTATTTT 683
Db      157  CTCCCAATAGCTGGGATTACTGCTGCTGCCACCAACGCGCCAGCTAAATTTTGTATTTT 216
QY      684  AGTAGAGACGGGGTTTTTGGCATGTTGCCAGGCTGGCCTTGAACCTCTGGCTCAAAACA 743
Db      217  AGTAGAGATGGGGTTTCAACATGTTGGCCAGGCTGGTCTTGAACCTCTGACCTCAGTGA 276
QY      744  TCACATGCTCGGCTCTCCAAAGTGTATGATTACAGCGGTGAGCCACCGTGCCTGGCC 803
Db      277  TCGGCTGCTCGGCTCTCCAAAGTGTGGGATTACAGCATGAGCCACCATGCTGACC 336
QY      804  TAAACATTTATCTTTTCTTTTGTGTT 828
Db      337  CTGTTCTTTCTTTTCTTTTCTTTCTT 361

RESULT 14
AW963663/c
LOCUS      727 bp mRNA linear EST 01-JUN-2000
DEFINITION EST375736 MAGE resequenes, MAGH Homo sapiens CDNA, mRNA sequence.
ACCESSION  AW963663
VERSION     AW963663.1 GI:8153499
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS     Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE       1 (bases 1 to 727)
JOURNAL     Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C.,
COMMENT     Holt, I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and
            Quackenbush, J.
            Assessment of gene expression patterns in a model of colon tumor
            metastasis using a 19,200 element cDNA microarray
            Unpublished (2000)
            Contact: John Quackenbush
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 3528
            Fax: 301 838 0208
            Email: johnq@tigr.org
            Plate: 190
            Seq primer: Reverse.
            Location/Qualifiers
            source          1..727
                        /organism="Homo sapiens"
                        /mol_type="mRNA"
                        /db_xref="taxon:9606"
                        /clone_lib="MAGE resequenes, MAGH"
                        /note="Vector: pBluescriptSKm"
ORIGIN
Query Match      19.6%; Score 230.6; DB 10; Length 727;
Best Local Similarity 78.8%; Pred. No. 2.7e-37;
Matches 275; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

QY      497  TCAACATTTATTTTATTTTATTTTATGACAGAGTCTCACTCTGTACCCAGGCTGGAGT 556
Db      563  TAAAAAATTTTATTTTATTTTATTTTATGACAGAGTCTCACTCTGTACCCAGGTTGGAGT 504
QY      557  GCAGTGGTGGCATCTCAGCTTACTGCAACCTCTGCTGCCAGGTTCAAGCATCTCATG 616
Db      503  GCAATGGCATGATCTTGTATCTGCAACCTCTGCGCTCCAGGTTCAAGTGAATCTCTCG 444
QY      617  CTTCCACCTCCCAAGTAGCTGGGACTACAGGCATGACCAACATGCCCAACTAATTTTGT 676
Db      443  CTTCAAGCTCCCAAGTAGCTGGGACTACAGGCATGACCAACATGCCCAACTAATTTTGT 384

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QY 677 TATTTTAGTAGAGACGGGTTTGGCATGTTCCAGGCTGCCCTTGAACCTCCTGGCCT 736
 Db 383 TATTTTAGCAGACGCGGTTTCATCATGTTGGCAGACTGTCTCGAATCCTGACCT 324
 QY 737 CAACAATCCACTTCCTCGGCTCCCAAGTGTATGATTACAGCGTGAGCCACCGTG 796
 Db 323 CAGGTGATCTGCCTCGCTCAGCTCCCAAGTGTGGAATTACAGCGTAAAGCCACCGTG 264
 QY 797 CTGGGCTTAACATTATCTTTCTTTGTTGTTGGAACTTTGAAATTAT 845
 Db 263 CCGGCGCTAAACTTTTAAATGTATACCTTTAGTTGGGTGAATTTTAT 215

RESULT 15
 A0180447 499 bp DNA linear GSS 23-OCT-1998
 LOCUS HS_3216_B2_C04_T7 CIT Approved Human Genomic Sperm Library D Homo
 DEFINITION sapiens genomic clone Plate=3216 Col=8 Row=F, genomic survey
 sequence.
 ACCESSION A0180447
 VERSION A0180447.1 GI:3577814
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 499)
 AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
 Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
 Hood,L.
 TITLE Sequence-tagged connectors: A sequence approach to mapping and
 scanning the human genome
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
 MEDLINE 99380589
 PUBMED 10449764
 COMMENT Contact: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Sequence Tagged Connector
 Plate: 3216 row: F column: 8
 Class: BAC ends
 High quality sequence stop: 499.
 Location/Qualifiers
 1..499
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="Plates3216 Col=8 Row=F"
 /sex="male"
 /clone_libs="CIT Approved Human Genomic Sperm Library D"
 /note="Organ: sperm; Vector: pBelBAC11; BAC Clones in
 E-Coli DH10B"

FEATURES
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 1..499
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="Plates3216 Col=8 Row=F"
 /clone_libs="CIT Approved Human Genomic Sperm Library D"
 /note="Organ: sperm; Vector: pBelBAC11; BAC Clones in
 E-Coli DH10B"

ORIGIN
 Query Match 19.6%; Score 230.4; DB 28; Length 499;
 Best Local Similarity 84.6%; Pred. No. 3.1e-37;
 Matches 258; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
 QY 502 CATTATTTTATTTTATTTTATTTAGACAGAGTCTCACTGTGACCCAGGCTGGAGTGCAGT 561
 Db 76 CATTATTTTATTTTATTTTATTTTGTGACAGAGTCTGCTGTGCGCCAGCTGGAGTGCAGT 135
 QY 562 GGTGCAATCTCAGCTTACTGCAACCTCTGCTGCGCAGGTTCAAGCGATTCTCATGCCCTCC 621
 Db 136 GGTGCAATCTTGGTGTACTGCAACCTCTGCTGCGCAGGTTCAAGCGATTCTCCTGCTCG 195
 QY 622 ACCCTCCCAAGTAGCTGGGACTACAGGATGACCAATGCCAATGCCAATTAATTTTGTATTT 681
 Db 196 CCCTCCCGAGTAGCTGGGATTACAGAGTGGCCACCATGCCCGGCTAATTTTGTATTT 255

QY 682 TTAGTAGAGACGGGTTTGGCATGTTGCCAGGCTGCCCTTGAACCTCCTGGCCTCAAC 741
 Db 256 TTAGTAAACAGGNGTTTGGCATGTTGGCAGGCTGGTCTTGAACCTCCTGGCCTCATTT 315
 QY 742 AATCAGCTTGCCTCGGCTCCCAAGTGTATGATTACAGCGCTGAGCCACCGTGCGCTGG 801
 Db 316 GATCCACTGCTTGGCCTCCCAAGTGTGGGATTACAGCATGAGCCACTGCACCCAG 375
 QY 802 CCTAA 806
 Db 376 CCTAA 380

RESULT 16
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 LOCUS AGENCOURT_10622246 NIH_MGC_107 Homo sapiens cDNA clone
 DEFINITION IMAGE:6731420 5', mRNA sequence.
 ACCESSION BU957399
 VERSION BU957399.1 GI:24186971
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 920)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: sgabbs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLCM3057 row: m column: 19
 High quality sequence stop: 609.
 Location/Qualifiers
 1..920
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6731420"
 /tissue_type="adenocarcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_libs="NIH_MGC_107"
 /note="Organ: breast; Vector: pOTE7; Site: 1: EcoRI;
 Site 2: XhoI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCAGAG(G). Library constructed by
 Ling Hong in the laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

FEATURES
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 1..920
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6731420"
 /tissue_type="adenocarcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_libs="NIH_MGC_107"
 /note="Organ: breast; Vector: pOTE7; Site: 1: EcoRI;
 Site 2: XhoI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCAGAG(G). Library constructed by
 Ling Hong in the laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

ORIGIN
 Query Match 19.6%; Score 230.4; DB 13; Length 920;
 Best Local Similarity 64.9%; Pred. No. 2.9e-37;
 Matches 355; Conservative 0; Mismatches 189; Indels 3; Gaps 1;
 QY 497 TCAAAACATTATTTTATTTTATTTTATTTAGACAGAGTCTCACTCTGTCCACCGGTGGAGT 556
 Db 158 TTAATATTATTTATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 217
 QY 557 GAGTGGTGCATCTCAGCTTACTGCAACCTCTGCTGCGCAGGTTCAAGCGATTCTCATG 616
 Db 218 GAGTGGCAGCATCTCGGCTCACTGCAACCTCGGCTCCAGGTTCAAGCGATTCTCTGT 277
 QY 617 CCTCCACCTCCCAAGTAGCTGGGACTACAGGATGACCAATGCCAATGAATTTTGT 676

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Db      278 CCTCAGCCTCCCAAGTAGCTGGATTACAGGCACCGCCACATGCTGGCTAAATTTTG 337
QY      677 TATTTTATGAGAGCGGGTTTGGCCATGTTGGCCAGGCTGGCTTGAACCTCTGGGCT 736
Db      338 TGTATTTAGTGAGACAGGATTCACCATGTTGGCCAGGCTGTTCTCGAATCTCTGACT 397
QY      737 CAACAACATCCACTTGCCTGGCTCCCAAGTGTGTATGATACAGGCTGAGCCACCGTG 796
Db      398 CGGTGATCCACCGGCTTGGTCTCCCAAGTGCAGGCTTACAGGCTGAGCCACCGTG 457
QY      797 CTGGGCTAAACATTTATCTTTCTTTGTTGGGAACCTTTGAAATTTATACAATGAATTA 856
Db      458 CCGGCGCTA--TCTACTATTAATCTTGAATTCCTGGCCACGCTTGTTCCTCCACACA 514
QY      857 TTGTTAACTGTCAATCCCTGCTGTGATGGAACACTGGGACTTCTTCCCTCTATCTAA 916
Db      515 GTGCTTGTGCTTATCTGCTCTCCATAGGATCCAGAGACATCTTCTCTCTCTCT 574
QY      917 CTGTATATTTGACAGTAAACACCGTACTTCTATCCCACTCTCTCTATCTCTCCACA 976
Db      575 CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 634
QY      977 ACCTCTGATACCTCAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1036
Db      635 CTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 694
QY      1037 TGTGAGT 1043
Db      695 CTGGAAT 701

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RESULT 17
AQ346434/c
LOCUS   RPCL11-101K7.TUB RPCL11 Homo sapiens genomic clone RPCL11-101K7,
DEFINITION genomic survey sequence.
ACCESSION AQ346434
VERSION   AQ346434.1 GI:4171330
KEYWORDS GSS.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens

```

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REFERENCE
AUTHORS Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter,J.C.
TITLE   Use of BAC End Sequences from Library RPCL11 for Sequence-Ready Map Building
JOURNAL Unpublished (1997)
COMMENT Other GSSs: RPCL11-101K7.TV
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@tigr.org
Clones are derived from the human BAC library RPCL11. For BAC library availability, please contact Pieter de Jong (pieter@jeong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/hungen/bac_end_search/bac_end_search.html
Seq primer: SP6
Class: BAC ends.
Location/Qualifiers
1. 705
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="GDB:7538646"
/db_xref="taxon:9606"
/clone="RPCL11-101K7"

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FEATURES
source

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/sex="Male"
/cell_type="Lymphocytes"
/clone_lib="RPCL11"
/note="vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCL11 Human Male BAC Library"

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ORIGIN

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Query Match      19.6%; Score 230.2; DB 28; Length 705;
Best Local Similarity 84.4%; Pred. No. 3.2e-37;
Matches 259; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY      508 TTTTATTTCTTTTATGACAGAGTCTCACTCTCTCCAGGCTGAGTGCATGGTCC 567
Db      327 TTTTATTTCTTTTATGAGATGAGTCTCACTCTATGCCCAGGCTGAAGTGCATGGTCC 268
QY      568 ATCTCAGCTTACTGCAACCTCTGCTGCGCAGGTTCAAGCGATTTCTCATGCTCCACCTCC 627
Db      267 ATCTCGGCTCACTGCAACCTCTGCTGCTCCAGGTTCAAGGATTTCTCTGCTCAGCTCC 208
QY      628 CAAGTAGCTGGGACTACAGCATGCACCAATGCCCAACTAATTTTGTATTTTATGTA 687
Db      207 CAAGTAGCTGGGATTACAGCGGTGTCACCATGCCAGCTAATTTTGTATTTTATGTA 148
QY      688 GAGACGGGGTTTGGCCATGTTGCCAGGCTGGCTTGAACCTCTGCGCTCAACATCCA 747
Db      147 GACACGGGGTTTGGCCATGTTGCCAGGCTGGCTTGAACCTCTGCGCTCAACATCTCT 88
QY      748 CTTGCTCTGGGCTCCCAAGTGTATTCATTTACAGGCTGAGCCACCGTGCCTGGCTTAA 807
Db      87 CTTGCTCTGAGCTCCCAAGTGTGCTGGATTACAGGTTGAGCCACTGACCTGGCTTGA 28
QY      808 CATTAT 814
Db      27 TTTGAAT 21

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RESULT 18

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BC035078/c
LOCUS   BC035078
DEFINITION Homo sapiens skeletrophin, mRNA (cdna clone IMAGE:5260457), with apparent retained intron.
ACCESSION BC035078
VERSION   BC035078.1 GI:23272436
KEYWORDS HTC.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2768)
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,P., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S., Loquellaro,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Faley,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S., Sanchez,A., Whitting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalls,D.E., Schneringer,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
12477932
2 (bases 1 to 2768)

```

TITLE

```

JOURNAL
MEDLINE
PUBMED
REFERENCE

```

AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (31-JUL-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
 Email: scapbs-remail.nih.gov
 cDNA Library Preparation: Mikhail J. Brownstein (NHGRI) & Shiraki Toshiyuki and Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
 contact: amadan@systemsbiology.org
 Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAX Plate: 73 Row: c Column: 6
 This clone has the following problem: retained intron.

FEATURES
 Location/Qualifiers
 1..2768
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5260457"
 /tissue_type="Brain_hippocampus"
 /clone_lib="NIH_MGC_95"
 /lab_host="DH10B"
 /note="Vector: pBluescript"

ORIGIN
 Query Match 19.6%; Score 230.2; DB 11; Length 2768;
 Best Local Similarity 81.0%; Pred. No. 2.8e-37;
 Matches 268; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 504 TTTATTTTATTTCTTTTACAGAGTCTCACTCTGTACCCAGGTGAGTGCAGTGG 563
 Db 2739 TTGTGTTTTTGTCTTTGACGAGTCTCACTCTGTACCCAGGTGAGTGCAGTGG 2680
 QY 564 TGCATCTCAGTCTACTGCACCTCTGCTGCCAGGTTCAGCGATTCTCATGCTCCAC 623
 Db 2679 CGAGTCTGTGCTCACTGCACCTCTGCTGCCAGGTTCAGCGATTCTCCACCTCAGC 2620
 QY 624 CTCCCAAGTAGCTGGGACTCAGGAGTGCACCAATGCCCAACTAAATTTTGTATTTT 683
 Db 2619 CTCCCAAGTAGCTGGGACTCAGGAGTGCACCAATGCCCAACTAAATTTTGTATTTT 2560
 QY 684 AGTAGAGAGGGGTTTCCCATGTTGCCAGCTGGCTTGAACCTCGGCTCAGCCTCAACAA 743
 Db 2559 AGTAGAGATGGGGTTTCCCATGTTGGCAAGGCTGGTCTCCAACTCTCTGGCCACAGTGA 2500
 QY 744 TCCACTTCCCTCGGCTCCCAAGTGTATGATTACAGCGCTGAGCCACCGTGGCTGGCC 803
 Db 2499 TCCTCCCACTGGGCTCACAAGTGTGGGATTACAGCGCTGAGCCACTGTGCTTGCT 2440
 QY 804 TAAACATTATCTTTCTTTGTGTTGGGAAC 834
 Db 2439 GGTGTTTTTCTTTTTTTTTTTTTTTTGTGAGAC 2409

RESULT 19
 AQ046370/c
 LOCUS RP11-34B11.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-34B11,
 DEFINITION genomic survey sequence.
 ACCESSION AQ046370
 VERSION AQ046370.1 GI:3315297
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 393)
AUTHORS Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C.
TITLE Use of BAC End Sequences for Sequence-Ready Map Building (1998)
JOURNAL Unpublished (1998)
COMMENT Contact: Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: mdadams@tigr.org
 Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
 Class: BAC ends.

FEATURES
 Location/Qualifiers
 1..393
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="GDB:7512706"
 /db_xref="taxon:9606"
 /clone="RPCI-11-34B11"
 /sex="Male"
 /cell_type="Lymphocytes"
 /clone_lib="RPCI-11"
 /note="Vector: pBACE3.6; Site 1: EcoRI; Site 2: EcoRI; RPCI11 Human Male BAC Library"

ORIGIN
 Query Match 19.5%; Score 229.8; DB 28; Length 393;
 Best Local Similarity 85.9%; Pred. No. 4.2e-37;
 Matches 255; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 508 TTTTATTTCTTTTGTAGACAGTCTCACTCTGTCAGGCTGAGTGCAGTGGTGC 567
 Db 304 TTTTATTTTCTTTTGTAGATGGAGTCTCACTCTATTTGCCAGGCTGAGTGCAGTGGTGC 245
 QY 568 ATCTCAGCTTACTGCAACTCTGCTGCCAGGCTCAAGCGATTCTCATGCTCCACCTCC 627
 Db 244 ATCTGGCTCACTGCAACTCTGCTGCCAGGCTCAAGCGATTCTCTGCTCAGCTCC 185
 QY 628 CAAGTAGCTGGAGCTACAGGAGTGCACCAATGCCCAACTAAATTTTGTATTTAGTA 687
 Db 184 CAAGTAGCTGGAGTACAGGAGTGCACCAATGCCCAACTAAATTTTGTATTTAGTA 125
 QY 688 GAGAGGGGTTTGGCATGTTGCCAGGCTGGCTTGAACCTCTGGCTCAAAACAATCCA 747
 Db 124 GACACGGGTTTGGCATGTTGCCAGGCTGGCTTGAACCTCTGGCTCAAGTATCT 65
 QY 748 CTTGCTTCGGCTCCCAAGTGTATGATTACAGCGTGGAGCCACCGTGGCTGGCT 804
 Db 64 CTTGCTTCAGCTCCCAAGTGTGGGATTACAGGTTGAGCCACTGCACCTGGCT 8

RESULT 20
 BZ611126/c
 LOCUS WHAPL87Ff Human MCF7 breast cancer cell line library (MCF7_1) Homo
 DEFINITION sapiens genomic clone MCF7_1-21P6, genomic survey sequence.
 ACCESSION BZ611126
 VERSION BZ611126.1 GI:31519687
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 808)
Volik S., Zhao S., Chin K., Brebner J.H., Herndon D.R., Tao Q.,
Kowbel D., Huang G., Lapuk A., Kuo W.-L., Magrane G., de Jong P.,
Gray J.W. and Collins C.
End-sequence profiling: Sequence-based analysis of aberrant genomes
Proc. Natl. Acad. Sci. U.S.A. 100 (13), 7696-7701 (2003)
12709111
12788976
Contact: Volik SV
Colin Collins' lab
UCSF Comprehensive Cancer Center
UCSF Box 0808, San Francisco, CA 94143-0808, USA
Tel: 415 502 7066
Fax: 415 502 5665
Email: svolik@cc.ucsf.edu
This clone is available from Amplicon Express
http://www.genomex.com
Class: BAC ends.

FEATURES
source
1..808
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="MCF7_1-21P6"
/sex="female"
/clone_lib="Human MCF7 breast cancer cell line library
(MCF7_1)"
/notes="Vector: pBCBAC1; Site 1: HindIII; This library was
constructed from MCF7 breast cancer cell line by Amplicon
Express (http://www.genomex.com) using their standard
procedure."

ORIGIN
Query Match 19.5%; Score 229.6; DB 28; Length 808;
Best Local Similarity 81.8%; Pred. No. 4.3e-37;
Matches 265; Conservative 0; Mismatches 59; Indels 0; Gaps 0;
QY 505 TTATTTTATCTTTTGTAGACAGAGTCTACTCTGTCACCCAGGCTGGAGTGCAGTGGT 564
Db 523 TTTTATTTTATTTTGTAGACAGAGTCTACTCTGTTGTCACCCAGGCTGGAGTGCAGTGGT 464
QY 565 GCCATCTCAGTCTACTGCAACTCTGCTGCAGGTTCAAGCGATCTCATGCTCCACC 624
Db 463 GCATCTCGGCTACTGCAACTCTGCTGCAGGTTCAATGATCTCTGCTCAGCC 404
QY 625 TCCCAAGTAGTGGGACTACAGGATGACACCAATGCCCAACTAAATTTTGTATTTTA 684
Db 403 TCCCAAGTAGTGGGATACAGGCGCCACACCAAGTCCAGCTAAATTTTATTTTA 344
QY 685 GTAGAGAGGGGTTTGGCATGTTGCCAGGCTGGCCTGAACTCCTGGCTCAACAAT 744
Db 343 GTAGAGACAGGTTTCAATGTTGGCAGGCTGCTTGAACCTCCTGACCTCAAGTGAT 284
QY 745 CCATCTGCTCGGCTCCCAAGTGTATGATTACAGGCTGAGCCACCGCTGCGCCT 804
Db 283 CTACTGCTTGGCTCCCAAGTGTAGGATTACAGGCTGAGCCACTGCTGCGGCC 224
QY 805 AAACATTATCTTTCTTTGTT 828
Db 223 AGAGGTAGATTCTGTTCAAGTGT 200

RESULT 21
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

A1133514
HA2127 Human fetal liver cDNA library Homo sapiens cDNA, mRNA
EST.
A1133514.1 GI:6360830
Homo sapiens (human)
Homo sapiens

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 651)
Yu, Y., Zhang, C., Luo, L., Ouyang, S., Li, W., Wu, J., Zhou, S., Liu, M.
and He, F.
Expression profile analysis of a human fetal liver cDNA library
Unpublished (1998)
Department of Hematology
Contact: Yongtao Yu
Beijing Institute of Radiation Medicine
27 Taiping Road, Beijing 100850, P.R.China
Tel: 0086-10-68159479
Fax: 0086-10-68214653
Email: yyt48@yahoo.com.

FEATURES
source
1..651
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="liver"
/dev_stage="fetal"
/lab_host="MC1061/p3"
/clone_lib="Human fetal liver cDNA library"
/note="Vector: pCDNA1"

ORIGIN
Query Match 19.5%; Score 229.2; DB 9; Length 651;
Best Local Similarity 82.0%; Pred. No. 5.3e-37;
Matches 264; Conservative 0; Mismatches 58; Indels 0; Gaps 0;
QY 486 TATCCATCATCAACAATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 545
Db 645 TATGTTTCTCAAAATCCCTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 586
QY 546 CAGGCTGGAGTGCAGTGGCCATCTCAGCTTACTGCAACCTCGCTGCCAGGTTCAAG 605
Db 585 CAGGCTGGAGTGCAGTGGGTGATCTCGGCTCAGTGCACATTTCTGTCCTCCAGGTTCAAG 526
QY 606 CGATTCTCATGCTCCACCTCCCAAGTAGCTGGGACTACAGGCATSCACCAATGCCCA 665
Db 525 TGATTCTCTGCTCAGGCTCCCAAGTAGTGGGATTACAGTGTGCACCGCCACGCCCA 466
QY 666 ACTAATTTTGTATTTTATTTAGTAGACGGGTTTGGCATGTTGCCAGGCTGGGCTTGA 725
Db 465 GCTAATTTTGTATTTTATTTAGTAGACGGGTTTGGCATGTTGCCAGGCTGGGCTTGA 406
QY 726 ACTCTGCGCTCAAAACAATCCACTTGCCTCGGCTCCCAAGTGTATGATTACAGGCT 785
Db 405 ACTCTGACCTCAGGGATCCACCTGCTTGGCTCCCAAGTGTGGGATTACAGGAT 346
QY 786 GAGCCACCGTGCCTGGCCTAAA 807
Db 345 GAGCCACCATGCTGGCCTGAA 324

RESULT 22
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AQ021621
CIT-HSP-2311P23.TF CIT-HSP Homo sapiens genomic clone 2311P23,
genomic survey sequence.
AQ021621
AQ021621.1 GI:3200357
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 452)
Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K.,
Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H.,
Simon, M. and Venter, J.C.
Use of a random BAC End Sequence Database for Sequence-Ready Map
Building (1998)

JOURNAL
COMMENT Unpublished (1998)
Other GSSs: CIT-HSP-2311P23.TR
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdamadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.

FEATURES
source Location/Qualifiers
1. 452
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="2311P23"
/sex="Male"
/cell_type="Sperm"
/clone_lib="CIT-HSP"
/note="Vector: pBelOBAC11; Site_1: HindIII; Site_2:
HindIII"

ORIGIN
Query Match 19.5%; Score 229; DB 28; Length 452;
Best Local Similarity 82.6%; Pred. No. 6e-37;
Matches 262; Conservative 0; Mismatches 55; Indels 0; Gaps 0;
QY 508 TTTTATTTTCTTTTAGACAGAGTCTCACTCTGTGACCCAGGCTGGAGTGCAGTGTGCC 567
Db 432 TTTTATTTTCTTTTAGACAGAGTCTCGCTCTGTGACACAGGCTGGAGTGCAGTGTGCA 373
QY 568 ATCTCAGCTTACTGCACTCTGCTGCGCAGGTTCAAGCGATTCTATGCTCCACTCC 627
Db 372 ATCTCAGCTCACTGCACTCCAGGCTCCAGGCTCCAGATTCAAGCGATTCTCTGCTCAGCCTCC 313
QY 628 CAAGTAGCTGGAGTACAGGATGCACCAATGCCCAACTAAATTTTGTATTTTAGTA 687
Db 312 CAAGTAGCTGGAATACAGATGTGCAACACAGCCAGCTAATTTTGTATTTTAGTA 253
QY 688 GAGACGGGTTTCCCATGTTGCCAGGCTGGCTTGAATCTCTGCGCTCAACAATCCA 747
Db 252 GAGATGGGTTTTCATGTTGGCAGGCTGTCTCAAACTCTCTGACCTCAAGTGATCTG 193
QY 748 CTTCGCTCGGCTCCCAAGGTTATGATTACAGGCTGAGCCACGCTGCTGCGCTTAA 807
Db 192 CTGCTTGGCTCCCAAGTCTGGGATTACAGGATGAGCCACCTGCGCCAGCCACCT 133
QY 808 CATTATCTTTTCTTTG 824
Db 132 CAGGTATTTTATAG 116

RESULT 23
AG167597 678 bp DNA linear GSS 09-JAN-2002
LOCUS Pan troglodytes DNA, clone: RP43-035L11.T7, genomic survey
DEFINITION sequence.
ACCESSION AG167597 GI:16697275
VERSION AG167597.1
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1
REFERENCE
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Tokoki, Y., Watanabe, H. and Sakaki, Y.
TITLE BAC end sequences of Library RPCI-43
JOURNAL Unpublished

REFERENCE 2 (bases 1 to 678)
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Tokoki, Y., Watanabe, H. and Sakaki, Y.
TITLE Direct Submission
JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
[E-mail: chimbeg@gsc.riken.go.jp, URL: http://bgp.gsc.riken.go.jp/,
Tel: 81-45-503-9111, Fax: 81-45-503-9170]
COMMENT Clones are derived from the chimpanzee BAC library RPCI-43. This BAC
end was generated during the R&D process and may have higher chance
of clone tracking errors.
PRIMERS
Sequencing: T7
LIBRARY
Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI.
FEATURES
source Location/Qualifiers
1. 678
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="RP43-035L11.T7"
/sex="male"
/cell_type="lymphocytes"
/clone_lib="RPCI-43 Chimpanzee Male BAC Library"

ORIGIN
Query Match 19.5%; Score 229; DB 29; Length 678;
Best Local Similarity 73.7%; Pred. No. 5.8e-37;
Matches 289; Conservative 0; Mismatches 103; Indels 0; Gaps 0;
QY 504 TTTATTTTATTTCTTTTAGACAGAGTCTCACTCTGTGACCCAGGCTGGAGTGCAGTGG 563
Db 255 TTTTATTTTCTTTTAGACAGAGTCTCACTCTGTGACCCAGGTTGGAGTACAGTGG 314
QY 564 TGCATCTCAGCTTACTGCAACCTCTGCTGCCAGGTTCAAGCGATTCTCATGCTCCAC 623
Db 315 CATGATCTCGGCTTACTGCAACTTCCGCTCTCTGGTTCAGGAGTCTCTCTGTTGAGC 374
QY 624 CTCCCAAGTAGCTGGAGTACAGGATGCACCAATGCCCAACTAAATTTTGTATTTT 683
Db 375 CTCCCAAGTAGCTGGAGTACAGGATGCACCAATGCCCAACTAAATTTTGTATTTT 434
QY 684 AGTAGACAGGGGTTTGGCCATGTTGCCAGTGTGCCAGTGTGCCCTTGAATCTCTGGCTCAACAA 743
Db 435 AGTAGACAGGGGTTTGGCCATGTTGGCCAGGAGGCTCTTGAACCCATGACCTCAGGTGA 494
QY 744 TCCACTTGCCTCGGCTCCCAAGTGTATGATTACAGCGTGAGCCACCGCTGCTGCC 803
Db 495 TCCGCCACTTTGGCTCTCCAGAGTGTAGATTTCAGGCGTGAGCCACACACTGGCC 554
QY 804 TAAACATTATCTTTCTTTGTTGGGAAGTCTTGAATTTATACAATGAATTTGTTAA 863
Db 555 TTTTCTCTATCTNNNTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT 614
QY 864 CTGTCATCTCCCTGCTGTGCTATGGAACACTG 895
Db 615 TGTTCCTCAAGCTAATATATGCAAGGGCGATG 646

RESULT 24
BH152879/c 504 bp DNA linear GSS 27-AUG-2001
LOCUS UP 297-17A T7 RPCI11 Human Male BAC Library Homo sapiens genomic
DEFINITION clone 297-17A, genomic survey sequence.
ACCESSION BH152879
VERSION BH152879.1 GI:15317004
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 504)
 Cheung,V.G., Dalrymple,H.L., Narasimhan,S., Watts,J., Schuler,G.,
 Raap,A.K., Morley,M. and Bruzel,A.
 A resource of mapped human bacterial artificial chromosome clones
 Genome Res. 9 (10), 989-993 (1999)
 99455100
 PUBMED
 10523527
 COMMENT
 Contact: Arcaro MA, Morley M, Burdick J, Cheung VG
 Department of Pediatrics
 University of Pennsylvania
 3516 Civic Center Blvd, ARC 516, Philadelphia, PA 19104, USA
 Tel: 215 590 2664
 Fax: 215 590 3709
 Email: mllennox@mail.med.upenn.edu
 Plate: 297 row: A column: 17
 Seq primer: T7
 Class: BAC ends.
 Location/Qualifiers
 1..504
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="297-17A"
 /sex="Male"
 /cell_type="Lymphocytes"
 /clone_lib="RPC111 Human Male BAC Library"
 /note="Vector: pBACe3.6; RPC111 Human Male BAC Library"

ORIGIN
 Query Match 19.4%; Score 228.6; DB 28; Length 504;
 Best Local Similarity 82.9%; Pred. No. 7.2e-37;
 Matches 261; Conservative 0; Mismatches 54; Indels 0; Gaps 0;
 QY 503 ATTATTTTATCTTTTATGACAGAGTCTCACTGTCTACCCAGGCTGAGTGCAGTG 562
 DB 501 ATTATATAAATTTTATTTTATGAGTGTCTGCTCTGTCACCCAGGCTGAGTGCAGTG 442
 QY 563 GTGCCATCTAGCTACTGCAACCTCTGCTGCCAGGTTCAAGGATCTCATGCTCCCA 622
 DB 441 GCACAATCTAGCTCACTGCAACCTCTGCCCTCCCGGTTCAAGCGATTTCTTGCCTCAG 362
 QY 623 CTCTCCCAAGTAGCTGGGACTACAGGCATGACCAACAATGCCCAACTAATTTTGTATTTT 682
 DB 381 CCTCCCAAGTAGCTGGGACTACAGGCATGTCACCACTGCTGCTAATTTTGTATTTT 322
 QY 683 TAGTAGACACGGGTTTGGCATGTTGCCAGGCTGCGCTTGAACACTCTGCGCTCAACA 742
 DB 321 TAACAGAGATGGGTTTGGCATGTTGCCAGGCTGATCTCAAACTCTCTGACCTCAGGTG 262
 QY 743 ATCCACTTGGCTCGGCTCCCAAAAGTGTATGATTACAGGCTGAGCCACCGTGCCTGGC 802
 DB 261 ATCCGCTGCTCGGCTCCCAAAAGTGTATGATTACAGGATAGCCATGAGCCACCGTGCCTAGC 202
 QY 803 CTAAACATTTATCTT 817
 DB 201 CTACTTTTATTTT 187

RESULT 25
 A0788367
 LOCUS
 DEFINITION
 HS 3135_A2 E11 MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3135 Col=22 Row=I, genomic survey sequence.
 A0788367
 GSS.
 A0788367.1 GI:5695991
 Homo sapiens (human)
 SOURCE
 Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 751)

REFERENCE
 A0788367
 LOCUS
 DEFINITION
 HS 3135_A2 E11 MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3135 Col=22 Row=I, genomic survey sequence.
 A0788367
 GSS.
 A0788367.1 GI:5695991
 Homo sapiens (human)
 SOURCE
 Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 751)

AUTHORS
 Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
 Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
 Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
 99380589
 MEDLINE
 10449764
 COMMENT
 Contact: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Clones may be purchased from Research Genetics (info@resgen.com).
 BAC end Web Server: http://www.htsc.washington.edu
 Plate: 3135 row: I column: 22
 Seq primer: M13 Reverse
 Class: BAC ends
 High quality sequence stop: 751.
 Location/Qualifiers
 1..751
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="Plate=3135 Col=22 Row=I"
 /sex="male"
 /clone_lib="CIT Approved Human Genomic Sperm Library D"
 /note="Organ: sperm; Vector: pBelobAC11; BAC Clones in E-Coli DH10B"

ORIGIN
 Query Match 19.4%; Score 228.4; DB 28; Length 751;
 Best Local Similarity 75.2%; Pred. No. 7.6e-37;
 Matches 297; Conservative 0; Mismatches 97; Indels 1; Gaps 1;
 QY 502 CATTTATTTTATCTTTTATGACAGAGTCTCACTGTCTACCCAGGCTGAGTGCAGT 561
 DB 188 CTTTCCTTTTATTTTATGACAGAGTCTCACTGTCTGCTCCAGGCTGAGTGCAGT 247
 QY 562 GTGCGCATCTAGCTTACTGCAACCTCTGCCCTGCCAGGTTCAAGCGATTTCTCATGCTCC 621
 DB 248 GGTGGCATCTCGCTCACTGCAACCTCTGCTCCAGGTTCAAGCGATTTCTCTGCTCA 307
 QY 622 ACTCTCCCAAGTAGCTGGGACTACAGGCATGACCAACAATGCCCAACTAATTTTGTATTT 681
 DB 308 GCGTCCCGAGTAGCTGGGACTATAGGCACGTGCCACCAACACCTGGCTAATTTCTGTATTT 367
 QY 682 TTAGTAGACACGGGTTTGGCATGTTGCCAGGCTGCGCTTGAACACTCTGCGCTCAAA 741
 DB 368 TTAGTAGACACAGGTTTACCATGTTGCCAGGCTGCTCGAACTCTCTGACTTCAGGT 427
 QY 742 AATCCACTTGCCTCGGCTCCCAAAAGTGTATGATTACAGGCTGAGCCACCGTGCCTGG 801
 DB 428 GATCCACCTGCTTGGCTCCCAAGTGTGGGATTAACAGGCATGAGCCACCGTGCCTGG 487
 QY 802 -CCTAAACATTTATCTTTTCTTTGTTGGGACATTTGAAATATACATGATTTATGTT 860
 DB 488 CCTGCACTCTCTATTTCTTCAATGGAATGTACCTTCTTCTGCTTCTGATTCCTTNC 547
 QY 861 TAACTGTATCTCCCTGCTGCTATGGAACACTG 895
 DB 548 TTCTTGGCCCTTTCTTCTCTGATCCCAAACTG 582

RESULT 26
 BE075068/c
 LOCUS
 DEFINITION
 PM1-BT0585-310100-002-g11 BT0585 Homo sapiens cDNA, mRNA sequence.
 BE075068
 BE075068.1 GI:84233577
 EST.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 324)
 AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
 Negai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
 Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,
 O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 PUBMED 10737800
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tit=at2=PM1-BT0595-310
 100-002-gli&t3=2000-01-31&t4=1)
 Seq primer: puc 18 forward
 High quality sequence stop: 323.
 Location/Qualifiers
 1. 324
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="BT0595"
 /note="Organ: breast; Vector: puc18; Site 1: SmaI; Site 2:
 SmaI; A mini-library was made by cloning products derived
 from ORBSTER PCR (U.S. Letters Patent application No.
 196,716 - Ludwig Institute for Cancer Research) profiles
 into the puc 18 vector. Reverse transcription of tissue
 mRNA and cDNA amplification were performed under low
 stringency conditions."
 ORIGIN
 Query Match 19.4%; Score 228.2; DB 10; Length 324;
 Best Local Similarity 81.9%; Pred. No. 9.1e-37; Indels 0; Gaps 0;
 Matches 263; Conservative 0; Mismatches 58;
 QY 510 TTTTATCTTTTACAGAGTCTCACTCTGTCAACCCAGGCTGGAGTGCAGTGGCCAT 569
 DB 322 TTTTATCTTTTACAGAGTCTCTGCTGTGACCCACCATGCTGAGTTCAGTGGCATGAT 263
 QY 570 CTGAGCTTACTGCAACCTCTGCTGCGAGGTTCAGGAGTTCATGCTCCACCTCCCA 629
 DB 262 GTCAGCTCACTGCAACCTCCGATTCAGGTTCCAGGTTCAGTTCATGCTTCACCTCTCA 203
 QY 630 AGTAGCTGGGACTACAGCATGACCAATGCCCCCACTAATTTTGTATTTAGTAGA 689
 DB 202 AATAGCTGGGATTACAGCTTGGCCACCAGCCATCTAATTTGTATTTTAGTAGG 143
 QY 690 GACGGGTTTGCATGTTGCCAGGTGGCTTTGAATCTGCGCTTCAAAATCACT 749
 DB 142 GACGGGTTTGCATGTTGGTGGGGGGTCTTGAATCTGCACTCAAGCGATCCACC 83
 QY 750 TGCTCGGCTCCCAAGAGTTATGATTACAGGGGTGAGCCACCGTCCCTGGCTAAACA 809
 DB 82 CGCTCGGCTCCCAAGAGTTATGATTACAGGGGTGAGCCACCGTCCCTGGCTAAACA 23
 QY 810 TTTATCTTTCTTTGTGTGG 830
 DB 22 GATCATTGTCTTCTTTATGG 2

RESULT 27
 A0535344
 LOCUS
 DEFINITION
 RPCI-11-356115-TV RPCI-11 Homo sapiens genomic clone
 RPCI-11-356115, genomic survey sequence.
 ACCESSION
 A0535344
 VERSION
 A0535344.1 GI:4847034
 KEYWORDS
 GSS.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 463)
 AUTHORS Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and
 Venter, J.C.
 TITLE Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
 Map Building
 JOURNAL Unpublished (1997)
 COMMENT Other GSSs: RPCI-11-356115 TJ
 Contact: Shaying Zhao, William Nierman, Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: hbs@tigr.org
 Clones are derived from the human BAC library RPCI-11. For BAC
 library availability, please contact Pieter de Jong
 (pieter@dejong.med.buffalo.edu). Clones may be purchased from
 BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
 Research Genet cs (info@resgen.com). BAC end search page:
 http://www.tigr.org/tldb/humgen/bac_end_search/bac_end_search.html.
 Seq primer: 27
 Class: BAC ends.
 Location/Qualifiers
 1. 463
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="GDB:7636526"
 /db_xref="taxon:9606"
 /clones="RPCI-11-356115"
 /sex="Male"
 /cell_type="Lymphocytes"
 /clone_lib="RPCI-11"
 /note="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI;
 RPCI11 Human Male BAC Library"
 ORIGIN
 Query Match 19.4%; Score 227.8; DB 28; Length 463;
 Best Local Similarity 81.9%; Pred. No. 1.1e-36;
 Matches 262; Conservative 0; Mismatches 58; Indels 0; Gaps 0;
 QY 505 TTTATTTTATCTTTTACAGAGTCTCACTCTGTCAACCCAGGCTGGAGTGCAGTGGT 564
 DB 81 TTTTATCTTTTACAGAGTCTCTGCTGTGACCCACCATGCTGAGTTCAGTGGCATGAT 140
 QY 565 GCCATCTCAGCTTACTGCAACCTCTGCTGCCAGGTTCACCGATTCTCATGCTCCACC 624
 DB 141 GTGATTCAGCTTACTGAAACCTCTGCTGCCAGGTTCACCGATTCTCTCTGCTCAGCC 200
 QY 625 TCCCAAGTAGCTGGAGTACAGGATGCACACATGCCCACTCAATTTTGTATTTTA 684
 DB 201 TCCCAAGTCTGTGGATTATAGGCACACATCACCATGCCCGACTAATTTTGTATTTTA 260
 QY 685 GTAGAGACGGGTTTGTGCATGTTGCCAGGCTGCGCTTGAACCTCCTGGCTCAACAAT 744
 DB 261 GTAGAGACAGGTTTACCATGTTGGCCAGGCTGGTCTTGAACCTCCTGAGCTAGGTAT 320
 QY 745 CCATTGCTCGGCTCCCAAGTGTATGATTACAGCGGTGAGCCACCGTCCCTGGCT 804
 DB 321 CCATCTCTCGGCTCCCAAGTGTGAGTATACAGCATGAACCACTGCGCTGGCCA 380

QY 805 ABAACATTTATCTTTCTTTG 824
 Db 381 CTGTCCATCNTTTTGTGTTG 400

RESULT 28
 LOCUS A1114733
 DEFINITION HAI332 Human fetal liver cDNA library Homo sapiens cDNA, mRNA
 sequence.
 ACCESSION A1114733
 VERSION A1114733.1 GI:6360078
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 593)
 AUTHORS Yu, Y., Zhang, C., Luo, L., Ouyang, S., Li, W., Wu, J., Zhou, S., Liu, M.
 and He, F.
 TITLE Expression profile analysis of a human fetal liver cDNA library
 JOURNAL Unpublished (1999)
 COMMENT Contact: fongtao yu
 Department of Hematology
 Beijing Institute of Radiation Medicine
 27 Taiping Road, Beijing 100850, P.R.China
 Tel.: 0086-10-68159479
 Fax: 0086-10-68214653
 Email: Yyf48@yahoo.com.

FEATURES
 source
 1..593
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /tissue_type="liver"
 /dev_stage="fetal"
 /lab_host="MC1061/P3"
 /clone_lib="Human fetal liver cDNA library"
 /note="Vector: pCDNA1"

ORIGIN
 Query Match 19.3%; Score 227.4; DB 9; Length 583;
 Best Local Similarity 78.0%; Pred. No. 1.3e-36;
 Matches 273; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

QY 497 TCAACATTTATTTTATCTTTTATGACAGAGTCTCACTCTGTCCACCCAGGCTGGAGT 556
 Db 226 TCAACATTTTATTTTATTTTATGAGTGGAGTCTCCCTCTGTCCACCCAGGCTGGAGT 285
 QY 557 GCAGTGTGCATCTCAGCTTACTGCAACCTCTGCCTGCCAGGTTCAAGCGATTCTCATG 616
 Db 286 GCAGTGTGCAGTCTCGACTCATTTGCACCTCCATCTTTGGGGTTCAAGTGATTCTCCTG 345
 QY 617 CCTCCACTCCAGTAGCTGGGACTACAGCATGACACATGCCCACTAATTTTGTG 676
 Db 346 CCTCAGGCTCTCAAGTAGCTGGGATTACAGCATGACACACCCAGGCCAGCTAATTTTG 405
 QY 677 TATTTTATGACAGCGGGTTTGGCCATGTGGCCAGGCTGGCTTGAACCTCTCGGCT 736
 Db 406 TATTTTATGACAGCGGGTTTCAACATGTGGCCAGGCTGGCTTGAACCTCTGACCT 465
 QY 737 CAACATATCCATCTGCTCGGCTCCCAAGTGTATGATPACAGGCGTGAGCCACCGTG 796
 Db 466 CAGGTGATCCACCCACCTTGGCCCTCTTGAAGTGTGGGATTATAGACGTGAGCCACTGTG 595
 QY 797 CCTGCGCTAAACATTTATCTTTCTTTCTGTGTGGAACTTTGAATTATA 846
 Db 526 CCTGCGCTAAAGAAATTTATTAATAAAATATCCAAATATGAGGAATA 575

RESULT 29
 LOCUS BC015230/c

LOCUS AL712182
 DEFINITION DKFZp686E1487_r1 686 (synonym: hicc3) Homo sapiens cDNA clone
 AL712182
 VERSION AL712182
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 592)
 AUTHORS Poustka, A., Wellenreuther, R., Mewes, H.W., Weil, B. and Wiemann, S.).
 TITLE EST (Poustka, A., Wellenreuther, R., Mewes, H.W., Weil, B. and Wiemann, S.)
 JOURNAL Unpublished (1999)
 COMMENT Contact: MIPS
 MIPS
 Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
 This is the 5' sequence of the clone insert
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
 Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;
 sequenced by DKFZ (German Cancer Research Center,
 Heidelberg/Germany) within the cDNA sequencing consortium of the
 German Genome Project.
 No sl sequence available.
 This clone (DKFZp686E1487) is available at the RZPD in Berlin.
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES
 source
 1..592
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="DKFZp686E1487"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="hicc3"
 /note="Vector: pTripEx2; Site_1: SfiIA; Site_2: SfiIB;
 cDNA-collection"

ORIGIN
 Query Match 19.3%; Score 227.4; DB 9; Length 592;
 Best Local Similarity 79.2%; Pred. No. 1.3e-36;
 Matches 270; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

QY 504 TTATTTTATCTTTTATGACAGAGTCTCACTCTGTCCACCCAGGCTGGAGTGGAGTGG 563
 Db 252 TTACTTTTATTTTATTTTATGACAGAGTCTCACTCTGTCTCAGGCTAGAGTGCAATGG 311
 QY 564 TGCCATCTCAGCTTACTGCAACCTCTGCCTGCCAGGTTCAAGCGATTCTCATGCTCCAC 623
 Db 312 TGCATCTCAGCTCACTGCAACTTCGGCTCCAGGTTCAAGCGATTCTCCTGCTCAGC 371
 QY 624 CTCCTCAGTAGCTGGAGTACAGGATGACACAAATGCCCACTAATTTTGTATTTT 683
 Db 372 CTCCTCAGTAGTGAACCTACAGGCGCCGCCACACCGCTGGCTTAATTTTGTATTTT 431
 QY 684 AGTAGAGAGCGGGTTTGGCCATGTGGCCAGGCTGGCTTGAACCTCTGGCTCAACAA 743
 Db 432 AGTAGAGAGCGGGTTTACCATTGTGGCCAGGCTGGTCTGAACTCTGACCTCAGGTGA 491
 QY 744 TCACCTTGCCTCGGCTCCCAAGTGTATGATTACAGGCGTGAGCCACCGTGCCTGCCC 803
 Db 492 TCCAAACCGCTCGGCTCCCAAGTGTATGAGATTACAGGCGTGAGGCACTGTGCCCGGCC 551
 QY 804 TAAACATTTATCTTTCTTTGTGGTGGAACTTTGAAATTA 844
 Db 552 CAGTTTTCTACTTCTATATGAGATGAATATATTTATTTTA 592

RESULT 30
 LOCUS BC015230/c
 BC015230 linear mRNA 1638 bp HTC 12-SEP-2002

DEFINITION Homo sapiens, clone IMAGE:3899552, mRNA.
 ACCESSION BC015230
 VERSION BC015230.1 GI:21955365
 KEYWORDS HTC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1638)
 AUTHORS Strausberg, R.
 TITLE Direct Submission
 JOURNAL Submitted (01-OCT-2003) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 COMMENT Contact: MGC help desk
 Email: cgaps-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome
 Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www-sbgc.stanford.edu>
 Contact: (Dickson, Mark) mcdepaxil.stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
 R. M.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAC Plate: 14 Row: 1 Column: 12
 This clone has the following problem: frame shifted.

FEATURES

source
 1..1638
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3899552"
 /tissue_type="pancreas, epithelioid carcinoma"
 /clone_lib="NIH_MGC_70"
 /lab_host="DH10B"
 /note="vector: pCMV-SPORT6"

ORIGIN

Query Match 19.3%; Score 227.4; DB 11; Length 1638;
 Best Local Similarity 84.7%; Pred. No. 1.1e-36;
 Matches 255; Conservative 0; Mismatches 46; Indels 0; Gaps 0;
 QY 504 TTTATTTTATCTTTTGTGACAGAGTCTCACTCTCTACCCAGGCTGGAGTGCAGTGG 563
 DB 1556 TTTTTTTTTTTTTTTGTGACAGAGTCTCACTCTCTACCCAGGCTGGAGTGCAGTGC 1497
 QY 564 TGGCATCTCAGCTTACTGCACACTCTCGCTGCCAGGTTCAAGGATCTCATGCTCCAC 623
 DB 1496 CACAATCTCAGCTCACAGCAACCTCCGCCCTCCAGGTTCAAGGATCTCTCTGCCTCAGT 1437
 QY 624 CTCCCAAGTAGCTGGGACTACAGGCATGCACCAATGCCCAACTAATTTTGTATTTT 683
 DB 1436 CTCCCAAGTAGCAGGATTACAGGCATGCACCACTGCCTGGCTACTTTTGTATTTT 1377
 QY 684 AGTAGACGGGGTTTGGCCATGTGTGCCAGGCTGGCTTGAATCTCGCCTCAACAA 743
 DB 1376 AGTAGACAGGGGTTTACCATGTGTGCCAGGCTGGCTTGAATCTCGCCTCAACAA 1317
 QY 744 TCCACTTGGCTCGGCTCCCAAGTGTATGATTACAGGCGTGAAGCCAGCTGCTGGCC 803
 DB 1316 TCCCCAGGCTCGGCTCCCAAGTGTATGATTACAGGCGTGAAGCCAGCTGCTGGCC 1257
 QY 804 T 804
 DB 1256 T 1256

RESULT 31
 AV756491/c
 LOCUS AV756491 BM Homo sapiens cDNA clone BMFAS04 5', mRNA sequence.
 DEFINITION AV756491
 ACCESSION AV756491
 VERSION AV756491.1 GI:10914339
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 551)
 AUTHORS Gu, J., Zhao, M., Huang, Q., Xu, X., Li, Y., Peng, Y., Song, H., Xiao, H.,
 Gu, F., Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z.,
 Zeng, L., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M.,
 Lu, G., Yang, Y., Gao, G., Wang, Z., Zhang, Q., Chen, S., Han, Z. and
 Chen, Z.
 TITLE Homo sapiens cDNA BM clones
 JOURNAL Unpublished (2000)
 COMMENT Contact: Zeguang Han
 Chinese National Human Genome Center at Shanghai
 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
 201203, P. R. China
 Tel: 86-21-50801919 (ex. 45)
 Fax: 86-21-50801922
 Email: hanzg@chgc.sh.cn
 This clone is available at CHGC in Shanghai.

FEATURES

source
 1..551
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="BMPAS04"
 /tissue_type="Bone marrow"
 /cell_type="CD34+ hematopoietic stem/progenitor cell"
 /lab_host="BM25.8"
 /clone_lib="BM"
 /note="Vector: pTriplex2; Site_1: sf1A; Site_2: sf1B"

ORIGIN

Query Match 19.3%; Score 227.2; DB 9; Length 551;
 Best Local Similarity 84.2%; Pred. No. 1.4e-36;
 Matches 256; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
 QY 504 TTTATTTTATCTTTTGTGACAGAGTCTCACTCTGTACCCAGGCTGGAGTGCAGTGG 563
 DB 391 TTTTTTTTTTTTTTTGTGACAGAGTCTCACTCTGTGTGCCAGGCTTGAGTGCAGTGG 332
 QY 564 TGGCATCTCAGTCTACTGCAACCTCTGCTGCCAGGTTCAAGCGATTCTCATGCTCCAC 623
 DB 331 CGCAATCTCAGTCTCACTGCAACCTCCGCCCTCCAGGTTCAAGCGATTCTCTGCTCAGC 272
 QY 624 CTCCCAAGTAGCTGGGACTACAGGCATGCACCAATGCCCAACTAATTTTGTATTTT 683
 DB 271 CTCCCTAGTAGCTGGGACTACAGGCATGGCGCACTACACCAGCTAATTTTGTATGTT 212
 QY 684 AGTAGACGGGGTTTGGCCATGTGTGCCAGGCTGGCTTGAATCTCTGGCTCAACAA 743
 DB 211 AGTAGAAGAGGTTTCAACATGTGTGCCAGGCTGGCTTGAATCTCTGCTCAAGTGA 152
 QY 744 TCCACTTGGCTCGGCTCCCAAGTGTATGATTACAGGCGTGAAGCCAGCTGCTGGCC 803
 DB 151 TCTGCCCTTTCAGCTTCCCAAGTGTGGGATTACAGGCATGAGCCACGCCCAGCC 92
 QY 804 TAAA 807
 DB 91 TAGA 88

RESULT 32

AV114557
 LOCUS AV114557
 DEFINITION HAI140 Human fetal liver cDNA library Homo sapiens cDNA, mRNA
 EST 11-NOV-1999

sequence.
 ACCESSION A1114557
 VERSION A1114557.1 GI:6359902
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 679)
 AUTHORS Yu,Y., Zhang,C., Luo,L., Ouyang,S., Li,W., Wu,J., Zhou,S., Liu,M. and He,F.
 TITLE Expression profile analysis of a human fetal liver cDNA library
 JOURNAL Unpublished (1998)
 COMMENT Contact: fongtao.yu
 Department of Hematology
 Beijing Institute of Radiation Medicine
 27 Taiping Road, Beijing 100850, P.R.China
 Tel: 0086-10-68159479
 Fax: 0086-10-68214653
 Email: yyt48@yahoo.com.

FEATURES
 source
 1..679
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /tissue_type="liver"
 /dev_stage="fetal"
 /lab_host="MC1061/P3"
 /clone_lib="Human fetal liver cDNA library"
 /note="Vector: pCDNA1"

ORIGIN
 Query Match 19.3%; Score 227.2; DB 9; Length 679;
 Best Local Similarity 76.9%; Pred. No. 1.4e-36;
 Matches 277; Conservative 0; Mismatches 83; Indels 0; Gaps 0;
 QY 504 TTTATTTTATCTTTTAGACAGAGTCTCACTCTGTCAACCAGGTGGAGTGCAGTGG 563
 Db 6 TTTTATTTTATTTTGTAGACGAGTCTCATCTGTCCCCAGGTGGAGTGCAGTGA 65
 QY 564 TGCATCTCAGTCTCACTCTGCTGCTGCGAGTTCAAGCATCTCATGCTCCAC 623
 Db 66 CGCGATCTCGGCTCACTGCAACCTCCACCTCCAGGTCAAGTGAATCTTCTGCTCAGC 125
 QY 624 CTCCTCAAGTAGCTGGAGTACAGGATGCACCAATGCCCACTAAATTTTGTATTTT 683
 Db 126 CTCCTGATAGTGGATTAGACATACCTCACATGCCAGTAAATTTTGTGTTTT 185
 QY 684 AGTAGACGGGTTTTGCCAGTTTGCACAGGTGGCTTGAATCTCTGGCTCAAAACA 743
 Db 186 AGTAGACAGAGGTTTCAACCATGTGGCCAGGCTGTGTCAACTCTCTGACCTCAGGTGA 245
 QY 744 TCCATCTCGCTCGGCTCCCAAGTGTATGATTACAGGCTGAGCCAGCTGCTGGCC 803
 Db 246 TCCAGTGCCTCGGCTCCCAAGTGTGGAATGCTGGAATGAGGCTGAGCCAGCTGCTGGCC 305
 QY 804 TAAACATTAATCTTTCTTTGTTGGAACTTGAATTAACAATTAATTTGTTAA 863
 Db 306 TGTATTTTGTGTTGTTTTTTTATTAATAAATCTTTTAAAAAGTGTATTTTCA 365

RESULT 33
 BM975412
 LOCUS 688 bp mRNA linear EST 21-FEB-2003
 DEFINITION UI-CF-EN1-acu-n-01-UI.s1 UI-CF-EN1 Homo sapiens cDNA clone
 UI-CF-EN1-acu-n-01-UI 3', mRNA sequence.
 ACCESSION BM975412
 VERSION BM975412.1 GI:19593003
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 MEDLINE
 PUBMED
 COMMENT

1 (bases 1 to 688)
 Bonaldo,M.F., Lennon,G. and Soares,M.B.
 Normalization and subtraction: two approaches to facilitate gene discovery
 Genome Res. 6 (9), 791-806 (1996)
 97044477
 8889548
 Contact: McCray, PB
 McCray Lab
 University of Iowa
 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
 Tel: 319 356 4866
 Fax: 319 356 7171
 Email: paul-mccray@uiowa.edu
 Tissue Procurement: Dr. M. J. Welsh, University of Iowa
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clones Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com) or from Open Biosystems (www.openbiosystems.com).
 The following repetitive elements were found in this cDNA sequence: 11-300, >ALU (matched complement)
 Seq primer: M13 FORWARD
 POLYA=Yes

FEATURES
 source
 1..688
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-CF-EN1-acu-n-01-0-UI"
 /tissue_type="Primary Lung Cystic Fibrosis Epithelial Cells"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
 /clone_lib="UI-CF-EN1"
 /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-CF-EN1 is a normalized cDNA library containing the following tissue(s): Primary Lung Cystic Fibrosis Epithelial Cells. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CTGCTCAGGT.
 TAG TISSUE=Human Lung Epithelial Cell Lines untreated LPS 6hr to LPS 24h
 TAG LIB=UI-CF-EN1
 TAG_SEQ=CTGCTCAGGT"

ORIGIN

Query Match 19.3%; Score 227.2; DB 12; Length 688;
 Best Local Similarity 76.1%; Pred. No. 1.4e-36;
 Matches 280; Conservative 0; Mismatches 88; Indels 0; Gaps 0;
 QY 504 TTTATTTTATCTTTTAGACAGAGTCTCACTCTGTCAACCAGGTGGAGTGCAGTGG 563
 Db 1 TTTTATTTTATTTTGTAGACGAGTCTCACTCTGCTCAACCAGGTGGAGTGCAGCGG 60
 QY 564 TGCATCTCAGTCTACTGCAACTCTGCTGCGAGTTCAACGGATTTCTCATGCTCCAC 623
 Db 61 CGAGATCTCTGCTCACTGCAACTCTCGCCCCCAGGTTCAAGCAATTTCTCTGCTCAGC 120
 QY 624 CTCCCAGTAGCTGGAGTACAGGATGCACCAATGCCCACTAAATTTTGTATTTT 683
 Db 121 CTCCTGTGTAATCTGGGATTACAGGGGCTGTGCCACACACACCCAGCTAAATTTTGTGTTTC 180
 QY 684 AGTAGACAGCGGTTTTTGGCATGTTGCCCGAGCTGGCCTTGAACCTCTGCTCCTCAACAA 743

Db CGCAGAGCGGGTTCCACCATGTTGGTCAGGCTGGTCTTGAGCTCTGACCTCAAGTGA 240
 QY TCCACTGCTCGGCTCCCAAGTGTATGATTACAGGGGTGAGCCACCGTGCCTGGCC 803
 Db TCCGCTGCTCGGCTCCCAAGCGTGGGAATACAGGGGTGAGCCACCGTGCCTGGCC 300
 QY TAAACATTATCTTTCTTTCTGTTGGAACTTTGAAATTATATAAATGAATTATTTGTTAA 863
 Db CGGAAGTAACTTCTATCTAGTTGAGTCATTTGGTATTTTAACTTTCACATTTCAGTAT 360
 QY CTGTCATC 871
 Db ATAGAATC 368

RESULT 34
 AG126146/c
 LOCUS Pan troglodytes DNA, clone: PTB-136J21.R, genomic survey sequence.
 DEFINITION
 ACCESSION AG126146
 VERSION AG126146.1 GI:16655311
 KEYWORDS GSS. Pan troglodytes (chimpanzee)
 SOURCE Pan troglodytes
 ORGANISM Pan troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 REFERENCE 1
 FUJIIYAMA, A., HATTORI, M., TOYODA, A., TAYLOR, T.D., YADA, T.,
 TOKOKI, Y., WATANABE, H. and SAKAKI, Y.
 BAC end sequences of library PTB
 UNPUBLISHED
 2 (bases 1 to 706)
 FUJIIYAMA, A., HATTORI, M., TOYODA, A., TAYLOR, T.D., YADA, T.,
 TOKOKI, Y., WATANABE, H. and SAKAKI, Y.
 Direct Submission
 TITLE Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
 1-22 Suenho-chou, Tsukumi-Ku, Yokohama, Kanagawa 230-0045, Japan
 (E-mail: chimpanzee@ric.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/
 Tel: 81-45-503-9111, Fax: 81-45-503-9170)
 Clones are derived from the chimpanzee BAC library PTB This BAC end
 was generated during the R&D process and may have higher chance of
 clone tracking errors.
 PRIMERS
 Sequencing: M13Rev
 LIBRARY
 Vector : pKS145
 R.Site 1 : SacI
 R.Site 2 : SacI.
 Location/Qualifiers
 1..706
 /organism="Pan troglodytes"
 /mol_type="genomic DNA"
 /db_xref="taxon:9598"
 /clone="PTB-136J21.R"
 /sex="male"
 /cell_type="lymphoblast"
 /clone_lib="PTB Chimpanzee Male BAC Library"

FEATURES
 source
 1..706
 /organism="Pan troglodytes"
 /mol_type="genomic DNA"
 /db_xref="taxon:9598"
 /clone="PTB-136J21.R"
 /sex="male"
 /cell_type="lymphoblast"
 /clone_lib="PTB Chimpanzee Male BAC Library"

ORIGIN
 Query Match 19.3%; Score 227.2; DB 29; Length 706;
 Best Local Similarity 77.8%; Pred. No. 1.4e-36;
 Matches 274; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

QY CATTTATTTTATCTTTTATGACAGAGTCTCACTCTGTACCCAGGCTGGAGTGCAGT 561
 Db CTTTTCGGTTTATTTTATGACAGAGGTTCTGCTGTACCCAGGCTGGAGTGCAGT 361
 QY GGTGCCATCTCAGCTTACTGCAACCTCTGCTGTCAGGTTCAAGCGATTCTCATGCTCC 621
 Db GGCAAGATCTCAGCTCACTGCAACCTCTGCTCTAGGTTCAAGAGAGGGGGCATGCTCA 301

QY 622 ACCTCCCAAGTAGCTGGGACTACAGGCATGCACCAATGCCCAACTAATTTTGTATTT 681
 Db 300 GCCTCCCAAGTAGCGGGATTACAGGCGTGACCATCATGCCAGCTGATTTTGTATTT 241
 QY 682 TTAGTAGAGAGGGGTTTGGCATGTTGCCAGAGCTGGCCTTGAACCTCCTGGCCTCAAC 741
 Db 240 TTAGTAGAGAGAGGGTTTCCACCATGTTGGCCAGAGCTGGTCTCAAAACTCTTGGCCTCATGT 181
 QY 742 AATCCACATTGCTCGGCTCCCAAAGTGTATGATTACAGCGGTGAGCCACCGTGCCTGG 801
 Db 180 GATCCACCGGCTGGCCTCCCAAAGTGTCTGGGATTACAGGCATGAGCCACCGTGCCTGG 121
 QY 802 CTAACAATTTATCTTTCTTTGTTGGGAACCTTTGAAATATATACAAATGAA 853
 Db 120 CTTTTTTCTTTCTTTCTTTTACTTTTAAATATAGGATGTGGCAGTGAA 69

RESULT 35
 AV754399/c
 LOCUS TP Homo sapiens cDNA clone TPGAGC06 5', mRNA linear EST 19-OCT-2000
 DEFINITION
 ACCESSION AV754399
 VERSION AV754399.1 GI:10912247
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 553)
 SONG, H., PENG, Y., GU, Y., YANG, Y., GAO, G., XIAO, H., XU, X., LI, N.,
 QIAN, B., LIU, F., QU, J., GAO, X., CHENG, Z., XU, Z., ZENG, L., XU, S.,
 GU, W., TU, Y., JIA, J., FU, G., REN, S., ZHONG, M., LU, G., HU, R., YE, M.,
 ZHANG, Q., HAN, Z., CHEN, Z. and CHEN, J.
 Homo sapiens TP library cDNA clones
 UNPUBLISHED (2000)
 CONTACT: Qinghua Zhang
 Shanghai Institute of Endocrinology, Rui-Jin Hospital
 197 Rui-Jin II Road, Shanghai 200025, P. R. China
 Tel: 86-21-64370045(ex.663332)
 Fax: 86-21-64743206
 Email: mshilms.stn.sh.cn
 This clone is available at Shanghai Hematology Institute in
 Shanghai.
 Chinese National Human Genome Center at Shanghai
 351 Guo Shouling Road, Zhangjiang Hi-Tech Park, Pudong.
 Location/Qualifiers
 1..553
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="TPGAGC06"
 /tissue_type="pituitary tumor"
 /dev_stage="Adult"
 /lab_host="BM25.8"
 /clone_lib="TP"
 /note="Vector: pTriplex2; Site_1: sf1A; Site_2: sf1B"

FEATURES
 source
 1..553
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="TPGAGC06"
 /tissue_type="pituitary tumor"
 /dev_stage="Adult"
 /lab_host="BM25.8"
 /clone_lib="TP"
 /note="Vector: pTriplex2; Site_1: sf1A; Site_2: sf1B"

ORIGIN
 Query Match 19.3%; Score 227; DB 9; Length 553;
 Best Local Similarity 84.1%; Pred. No. 1.5e-36;
 Matches 265; Conservative 0; Mismatches 49; Indels 1; Gaps 1;

QY 504 TTTATTTTATCTTTTATGACAGAGTCTCACTCTGTACCCAGGCTGGAGTGCAGTGG 563
 Db 416 TTTTATTTTATCTTTTATGATGGAGTCTCACTCTGTACCCAGGCTGGAGTGCAGTGG 357
 QY 564 TGGCATCTCAGCT-TACTGCAACCTCTGCTGCGAGGTTCAAGCGATTCTCATGCTCCA 622
 Db 356 TGGCATCTCAGCTCAACTGCGAGCTCTGCTCCCGAGGTTCAAGTATCTCTGCTCCTCAG 297
 QY 623 CTCTCCCAAGTAGCTGGGACTACAGGCATGACCAATGCCCAACTAATTTTGTATTT 682
 Db 296 CTCTCCCAAGTAGCTGGGATTACAGGCGCCNCCNCCATGCCAGCTAATTTTGTATTT 237

QY	596	CAGGTTCAAGCGATTCTCATGCTCTCCACCTCCCAAGTAGCTGGAGCTACAGGCGATGCACC	655
Db	302	CAGGTTCAAGCTATTCTCTTGCTCGACGCTCCCAAGTAGCTGAGATTACAGGACCCACC	361
QY	656	ACAATGCCCAACTAATTTTTGTATTTTTAGTAGAGACGGGTTTTGCCATGTTGCCCAGG	715
Db	362	ACCATGCTGGCTAAATTTTGTATTTTTAGTAGAGTGGGATTTACCATGTTGGCCAGG	421
QY	716	CTGGCTTTGAATCTCTGGGCTCAAAACAATCCACTTCCTCGGCTCCCCAAGATGTTATGA	775
Db	422	CTGGTCTCGAACTCCCTGAGCTCAGTCAAGTATCCACTGCTCAGGCTCCCAAGTGTCTGGA	481
QY	776	TTACAGCGTGAAGCCACCGTGCCTGCCTGACCTAAACATTTATCTTT	818
Db	482	TTACAGCATGACCCACCGTACCTGCGCGCTCGGTTTTAATTT	524
RESULT 37			
AG161060/c			
LOCUS	AG161060	608 bp	DNA linear GSS 09-JAN-2002
DEFINITION	Pan troglodytes DNA, clone: RP43-027B06.TU, genomic survey		
ACCESSION	AG161060		
VERSION	AG161060.1		
KEYWORDS	GI:16690738		
SOURCE	GSS.		
ORGANISM	Pan troglodytes (chimpanzee)		
REFERENCE	Pan troglodytes		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.		
TITLE	1 Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,		
JOURNAL	Totoki,Y., Watanabe,H. and Sakaki,Y.		
REFERENCE	BAC end sequences of Library RPCI-43		
AUTHORS	Unpublished		
TITLE	2 (bases 1 to 608)		
JOURNAL	Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,		
REFERENCE	Totoki,Y., Watanabe,H. and Sakaki,Y.		
AUTHORS	Direct Submission		
TITLE	Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical		
JOURNAL	and Chemical Research (RIKEN), Genomic Sciences Center (GSC);		
REFERENCE	1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan		
AUTHORS	(E-mail:chimps@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/.		
TITLE	Tel:81-45-503-9111, Fax:81-45-503-9170)		
JOURNAL	Clones are derived from the chimpanzee BAC library RPCI-43 This BAC		
REFERENCE	end was generated during the R&D process and may have higher chance		
AUTHORS	of clone tracking errors.		
PRIMERS	Sequencing: TJ		
LIBRARY	Vector : pBACe3.6		
FEATURES	R.Site 1 : EcoRI		
source	R.Site 2 : EcoRI		
Location/Qualifiers	1. .608		
/organism="Pan troglodytes"	/mol_type="genomic DNA"		
/db_xref="taxon:9598"	/clone="RP43-027B06.TU"		
/sex="male"	/cell_type="lymphocytes"		
/clone_lib="RPCI-43 Chimpanzee Male BAC Library"			
ORIGIN			
Query Match	19.3%;	Score 227;	DB 29; Length 608;
Best Local Similarity	80.4%;	Pred. No. 1.5e-36;	
Matches	266;	Conservative	0; Mismatches 65; Indels 0; Gaps 0;
QY	491	ATCACATCAACAATTATTTTATCTTTTATGACAGAGTCTCATCTGTACCCAGGC	550
Db	390	AACAGATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT	331
QY	551	TGGAGTGCAGTGGTGCATCTCAGCTTACTGCAACCTCTGCTGCCAGGTTCAAGGATT	610

Db 530 TGTGTTTCTTTTGTGAGACAGATCTCACTGTGTCACCCAGGCTGGAGTGCATGG 471
 QY 564 TGCATCTCAGCTTACTGCAACCTCTGCTGCCAGGTTCAAGCGATTTCTCATGCTCCAC 623
 Db 470 CATGATCTGACTCACTGCTACTCTCGCTCCAGGTTCAAGTATTTCTCTGCTCAGC 411
 QY 624 CTCCCAAGTAGCTGGAGTACAGGATGACACCAATGCCCACTAATTTTGTATTTT 683
 Db 410 CTCCCAAGTAGCTGGAGTACAGGATGACACCAATGCCCACTAATTTTGTATTTT 351
 QY 684 AGTAGAGACGGGTTTTCGCATGTTGCCAGGCTGGCTTGAATCTCTGGCTCAACAA 743
 Db 350 AGCAGAGACGGGTTTTCATGTTGGCAGACTGTCTCGAATCTCTGACTCAGGTGA 291
 QY 744 TCCACTTGCCTCGGCTCCCAAGTGTATGATTACAGCGGTGAGCCACCGTCTGGCC 803
 Db 290 TCTGCTGCTCAGCCTCCCAAGTGTGGAATTACAGCGGTGAGCCACCGTCTGGCC 231
 QY 804 TAAACATTTATCTTTCTTGTGTTGGGAACCTTTGAATTTAT 845
 Db 230 TAAACATTTTAAATGATATCTTTAGTTGGTGAATTTTAT 189

RESULT 40
 BX489032
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

DXZP686L02275_r1 686 (synonym: hlcc3) Homo sapiens CDNA clone
 DXZP686L02275 5', mRNA sequence.
 BX489032
 BX489032.1 GI:31955172
 EST.
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 447)
 Wambutt,R., Heubner,D., Mewes,H.W., Weil,B., Amid,C., Oeanger,A.,
 Fobo,G., Han,M. and Wiemann,S.
 EST (Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., et al.)
 Unpublished (2003)
 Contact: MIPS

MIPS
 Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
 This is the 5' sequence of the clone insert
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
 Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
 sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing
 consortium of the German Genome Project.

No si sequence available.
 This clone (DXZP686L02275) is available at the RZPD in Berlin.
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES
 source
 1..447
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="DXZP686L02275"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="hlcc3" (synonym: hlcc3)
 /note="Vector: pRipEx2; Site_1: sfliA; Site_2: sfliB;
 cDNA-collection"

ORIGIN
 Query Match 19.3%; Score 226.6; DB 13; Length 447;
 Best Local Similarity 76.7%; Pred. No. 1.9e-36;
 Matches 277; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 504 TTTATTTTATCTTTTATAGACAGATCTCACTGTGTCACCCAGGCTGGAGTGCATGG 563
 Db 30 TTTTCTCTTTTGTGAGACAGATCTCGCTCTGTGTCACCCAGGCTGGAGTGCATGG 89

QY 564 TGCCATCTCAGCTTACTGCAACCTCTGCTGCCAGGTTCAAGCGATTTCTCATGCTCCAC 623
 Db 90 CGGATCTCGGCTCACTGCAAACTCCACCTCCGGGTTCAAGCAGTTCTCTGCTCAGC 149
 QY 624 CTCCCAAGTAGCTGGAGTACAGGATGACACCAATGCCCACTAATTTTGTATTTT 683
 Db 150 CTCCCAAGTAGCTGGAGTACAGGATGACAGGCTCGGCCACCATGCCCAATTTTGTATTTT 209
 QY 684 AGTAGAGACGGGTTTTCGCATGTTGCCAGGCTGGCTTGAATCTCTGGCTCAACAA 743
 Db 210 AGTAGAGATGGGTTTTCACCATGTTGCCAGGCTGTCTCGAATCTCTGACTCAGGTGA 269
 QY 744 TCCACTTGCCTCGGCTCCCAAGTGTATGATTACAGCGGTGAGCCACCGTCTGGCC 803
 Db 270 TCCACTCGCTCGGCTCCCAAGTGTGGAATTATAGGATGCGGCCACCATGCCCGGCC 329
 QY 804 TAAACATTTATCTTTCTTGTGTTGGGAACCTTTGAATTTATTTTATTTTGA 863
 Db 330 GGCTTATGATTAAACATGAATTTGTTTATTTCTGGAATTTTCCACATATTTTGA 389
 QY 864 C 864
 Db 390 C 390

RESULT 41
 CB296753
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

12B22011_rev_1_C11_r_086.ab1 Chimpanzee brain library Koo's Pan
 troglodytes cDNA clone 12B22011_rev_1_C11_r_086.ab1 5', mRNA
 sequence.
 CB296753
 CB296753.1 GI:28622183
 EST.
 Pan troglodytes (chimpanzee)
 Pan troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 1 (bases 1 to 580)
 Hellmann,I., Zollner,S., Enard,W., Ebersberger,I., Nickel,B. and
 Paabo,S.
 Selection on human genes as revealed by comparisons to chimpanzee
 cDNA

Genome Res. (2003) In press
 Contact: Paabo S
 Evolutionary Genetics
 Max-Planck-Institute for evolutionary Anthropology
 Deutscher Platz 6, 04103 Leipzig, Germany
 Tel: +49-(0)-341-3550 500
 Fax: +49-(0)-341-3550 555
 Email: paabo@eva.mpg.de
 Seq primer: M13 reverse.

FEATURES
 Location/Qualifiers
 1..580
 /organism="Pan troglodytes"
 /mol_type="mRNA"
 /db_xref="taxon:9598"
 /clone="12B22011_rev_1_C11_r_086.ab1"
 /sex="male"
 /tissue_type="brain, presumably cortex"
 /dev_stage="adult"
 /lab_host="Epicurian Coli (TM) XL-10-Gold"
 /clone_lib="Chimpanzee brain library Koo's"
 /note="Vector: pUCHI; Site 1: SfII-A; Site 2: SfII-B; The
 library was prepared using the SMART cDNA library
 construction kit (Clontech), doing only primer extension,
 but not PCR amplification of the cDNA. The only deviation
 from the published protocol was that we cloned the cDNA
 into a plasmid vector."

ORIGIN
 Query Match 19.3%; Score 226.6; DB 14; Length 580;
 Best Local Similarity 83.9%; Pred. No. 1.8e-36;

Matches 256; Conservative 0; Mismatches 49; Indels 0; Gaps 0;
 QY 504 TTTATTTTATTTCTTTTACAGAGTCTCTCTGTCACCCAGGCTGAGTGCAGTGG 563
 Db 41 TTCACTTTTTTTTTTTTGGACAGAGTCTCACTCTGTCAACCCAGGCTGAGTGCATGG 100
 QY 564 TGCCATCTCAGCTTACTGCAACCTCTGCTGCCAGGTTCAAGCGATTCTCATGCTCCAC 623
 Db 101 CATCATCTCGCTCACTGCAACCTCTGCTGCCAGGTTCAAGTATTCTCTGCCICAGC 160
 QY 624 CTCCCAAGTAGCTGGAGTCAAGGATGACACCAATGCCCAACTAATTTTGTATTTT 683
 Db 161 CTCTCGAGTAGCTGGAGTCAAGGATGACACCACTGCCAGCTAATTTTCATATTTT 220
 QY 684 AGTAGAGAGCGGGTTTCCCATGTTGCCAGGCTGGCTTGAATCTCTGCTGCCCAACAA 743
 Db 221 AGTAGAGAGCGGGTTTCACTTTGTGGCAGGCTGGTCTCAAACTCTGACATCAAGTGA 280
 QY 744 TCCACTTGCCTCGGCTCCCAAGTGTATGATTACAGGCGTGAGCCACCGTGCTGGCC 803
 Db 281 TCCGCTGCTTGGCTTCCCAAGCGTGGGATTACAGGCGTGAGCCACCGCGCGCGCC 340
 QY 804 TAAAC 808
 Db 341 TGAAC 345

RESULT 42
 AG178621/c
 LOCUS
 DEFINITION Pan troglodytes DNA, clone: RP43-050K09.TJ, genomic survey
 sequence.
 ACCESSION AG178621
 VERSION AG178621.1 GI:16708301
 KEYWORDS GSS.
 SOURCE Pan troglodytes (chimpanzee)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
 1
 Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
 Tokoki,Y., Watanabe,H. and Sakaki,Y.
 BAC end sequences of Library RPCI-43
 2 (bases 1 to 676)
 Unpublished
 Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
 Tokoki,Y., Watanabe,H. and Sakaki,Y.
 Direct Submission
 Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
 1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 (E-mail:chimbases@sc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/
 Tel:81-45-503-9111, Fax:81-45-503-9170)
 Clones are derived from the chimpanzee BAC library RPCI-43 This BAC
 end was generated during the R&D process and may have higher chance
 of clone tracking errors.
 PRIMERS
 Sequencing: TJ
 LIBRARY
 Vector : pBACe3.6
 R.Site 1 : EcoRI
 R.Site 2 : EcoRI.
 Location/Qualifiers
 1. 676
 /organism="pan troglodytes"
 /mol_type="genomic DNA"
 /db_xref="taxon:9598"
 /clone="RP43-050K09.TJ"
 /sex="male"
 /cell_type="lymphocytes"
 /clone_lib="RPCI-43 Chimpanzee Male BAC Library"

FEATURES

source
 1. 676
 /organism="pan troglodytes"
 /mol_type="genomic DNA"
 /db_xref="taxon:9598"
 /clone="RP43-050K09.TJ"
 /sex="male"
 /cell_type="lymphocytes"
 /clone_lib="RPCI-43 Chimpanzee Male BAC Library"

ORIGIN

Query Match 19.3%; Score 226.6; DB 29; Length 676;
 Best Local Similarity 82.7%; Pred. No. 1.8e-36;
 Matches 259; Conservative 0; Mismatches 54; Indels 0; Gaps 0;
 QY 505 TTATTTTATTTCTTTTACAGAGTCTCTCTGTCACCCAGGCTGAGTGCAGTGGT 564
 Db 406 TTGTTGTTGTTGTTTATTTAGACAGAGTCTCACTCTGTGCCAGGCTGAGTGCATGGC 347
 QY 565 GCATCTCAGCTTACTGCAACCTCTGCTGCCAGGTTCAAGCGATTCTCATGCTCCACC 624
 Db 346 GCAATCTCGGCTCACTGCAACCTCTGCTCGGCTCAAGTATTCTCTGCCCTCAGCC 287
 QY 625 TCCCAAGTAGCTGGAGTACAGGATGACCAATGCCCAACTAATTTTGTATTTT 684
 Db 286 TCCTCAGTAGCTAGGCTTACAGGACGACCAACACCGCCAGCTAATTTTGTATTTT 227
 QY 685 GTAGAGAGCGGGTTTGGCATGTTGCCAGGCTGGCTTGAATCTCTGCTGCCCAACAAT 744
 Db 226 GTAGAGAGCGGGTTTACCATGTTGCCAGGCTGGTCTTGAATCTCTGACCTCAGTGTAT 167
 QY 745 CCACCTTGCCTCGGCTCCCAAGTGTATGATTACAGGCGTGAGCCACCGTGCTGGCCT 804
 Db 166 CCACCGCTCAGCCTCCCAAGTGTCTGGGTTTACAGGCGTGAGCGGCTGGCGCTGCTT 107
 QY 805 AAACATTTTATCTT 817
 Db 106 ACAGGGTTTTTTT 94

RESULT 43
 AQ543621/c
 LOCUS
 DEFINITION RPCI-11-346H5.TV RPCI-11 Homo sapiens genomic clone RPCI-11-346H5,
 genomic survey sequence.
 ACCESSION AQ543621
 VERSION AQ543621.1 GI:4873905
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 681)
 Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and
 Venter,J.C.
 Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
 Map Building
 Unpublished (1997)
 Other GSSs: RPCI-11-346H5.TJ
 Contact: Shaying Zhao, William Nierman, Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: hbs@tigr.org
 Clones are derived from the human BAC library RPCI-11. For BAC
 library availability, please contact Pieter de Jong
 (pieter@dejong.med.buffalo.edu). Clones may be purchased from
 BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
 Research Genet cs (info@resgen.com). BAC end search page:
 http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
 Seq primer: T7
 Class: BAC ends.
 Location/Qualifiers
 1. 681
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="GDB:763262"
 /db_xref="taxon:9606"
 /clone="RPCI-11-346H5"
 /sex="Male"
 /cell_type="Lymphocytes"
 /clone_lib="RPCI-11"

FEATURES

source
 1. 681
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="GDB:763262"
 /db_xref="taxon:9606"
 /clone="RPCI-11-346H5"
 /sex="Male"
 /cell_type="Lymphocytes"
 /clone_lib="RPCI-11"


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/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPEC111 Human Male BAC Library"

ORIGIN
Query Match      19.3%; Score 226.6; DB 28; Length 681;
Best Local Similarity 82.7%; Pred. No. 1.8e-36;
Matches 259; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY 504 TTTATTTTATCTTTTATAGACAGAGTCTCACTCTGTCAACCCAGGCTGGAGTGCAGTGG 563
    |||
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RESULT 44
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LOCUS      60302244F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5192867 5',
DEFINITION mRNA sequence.
ACCESSION BI752166
VERSION    BI752166.1 GI:15743744
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 712)
AUTHORS   NIH-MGC http://mgi.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT    Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: Life Technologies, Inc.
           cDNA Library Preparation: Life Technologies, Inc.
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Incyte Genomics, Inc.
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
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               /clone_lib="NIH_MGC_114"
           /note="Organ: brain; Vector: pcwv-sport6; Site_1: NotI;
           Site_2: EcoRV (destroyed); RNA source anonymous pool of 6
           male brains, age range 23-27 yo. Library is oligo-dr
           primed and directionally cloned (EcoRV site is destroyed
           upon cloning). Average insert size 1.5 kb, insert size

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range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(invitrogen). Research Genetics tracking code 019. Note:
this is a NIH_MGC Library."

ORIGIN
Query Match      19.3%; Score 226.6; DB 12; Length 712;
Best Local Similarity 78.6%; Pred. No. 1.8e-36;
Matches 271; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

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QY 552 GAGTGCAGTGGTCCCATCTCACTTACTGCAACCTCTGCTGCCAGGTTCAAGCGATTC 611
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QY 612 TCATGCTCCACCTCCCAAGTAGCTGGACTACAGCATGCCACCAATGCCCCAATAT 671
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QY 732 GGCTCAACAACATCCACTTGCCTCGGCTCCCAAGTGTATGATTACAGGCTGAGCCA 791
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QY 792 CCGTGGCTGGCTAAACATTTATCTTTTCTTTTGTGTGGAACTT 836
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RESULT 45
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LOCUS      AGENCOURT 16386158 NIH_MGC_229 Homo sapiens cDNA clone
DEFINITION IMAGE:30721940 5', mRNA sequence.
ACCESSION CK005530
VERSION    CK005530.1 GI:38531572
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 631)
AUTHORS   NIH-MGC http://mgi.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT    Contact: Daniela S. Gerhard, Ph.D.
           Office of Cancer Genomics
           National Cancer Institute / NIH
           Bldg. 31 Rm10A07 Bethesda, MD 20892
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: Professor Mikliss Palkovits
           cDNA Library Preparation: Michael Brownstein / Ted Usdin
           Laboratory
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Agencourt Bioscience Corporation
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: NDCM270 row: m column: 21
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               /clone="IMAGE:30721940"
               /tissue_type="Human Brain - Frontal Cortex"

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Class: BAC ends
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 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="Plate-1149 Col=4 Row=E"
 /sex="male"
 /clone_lib="RPC1-11 Human Male BAC Library"
 /note="vector: pBACe3.6; Site1: EcoRI; Site2: EcoRI;
 Male blood DNA was isolated from one randomly chosen donor
 and partially digested with a combination of EcoRI and
 EcoRI Methylase. Size selected DNA was cloned into the
 pBACe3.6 vector at EcoRI sites"

ORIGIN

Query Match	19.2%	Score 226.2	DB 28	Length 828
Best Local Similarity	81.8%	Pred. No. 2.1e-36		
Matches 261	Conservative 0	Mismatches 58	Indels 0	Gaps 0

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Db	336		
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Db	396		
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Db	456		
QY	684	AGTAGAGCGGGGTTTTCATGTTGCCAGGCTGGCCCTTGAAGTCTCCTGGCTCAAAACA	743
Db	516		
QY	744	TCCACTTGCCTCGGCTCCCAAGTGTATGATTACAGGCGTGAGCCACCGCTGCTGGCC	803
Db	576		
QY	804	TAAACATTATCTTTCTT	822
Db	636		

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 Job time : 2928 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 16, 2004, 17:43:13 ; Search time 4560 Seconds
(without alignments)
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Title: US-10-063-736-129
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues 6940544
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: gb.ov.*
6: gb.pat.*
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10: gb.ro.*
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34: em.htg.pln.*
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38: em.sy.*
39: em.htgo.hum.*
40: em.htgo.mus.*
41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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		Match	Length				
1	1177	100.0	1177	6	AX092398	Sequence	
2	1177	100.0	1177	6	AX358958	Sequence	
3	1177	100.0	1177	6	AX362451	Sequence	
4	1177	100.0	1177	6	AX376314	Sequence	
5	1177	100.0	1177	6	AX454686	Sequence	
6	1177	100.0	1177	6	AX491164	Sequence	
7	1177	100.0	1177	9	AY358613	Homo sapi	
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C	14	370.6	31.5	168283	2	AC027633	Homo sapi
C	15	351.8	29.9	162145	9	AC131572	Homo sapi
16	351	29.8	136124	9	HS394P21	Human DNA	
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C	19	349.6	29.7	30826	9	AL807743	Human DNA
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C	28	342.6	29.1	160915	2	AP001084	Homo sapi
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C	30	342.6	29.1	171978	2	AC009669	Homo sapi
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C	34	337.4	28.7	184541	9	AC011405	Homo sapi
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C	38	332.8	28.3	107685	9	EX679664	Human DNA
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43	330	28.0	175842	9	AL731547	Human DNA	
44	329.6	28.0	32074	9	AC104533	Homo sapi	
45	329.4	28.0	140091	9	AL445684	Human DNA	

ALIGNMENTS

RESULT 1
AX092398
LOCUS
DEFINITION Sequence 129 from Patent WO0116318.
ACCESSION AX092398
VERSION AX092398.1 GI:13444513
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Eaton, D.L., Filvaroff, E., Gerritsen, M.E., Goddard, A.,
Gadowski, P.J., Grimaldi, C.J., Gurney, A.L., Watanabe, C.K. and
Wood, W.I.

AX092398 1177 bp DNA linear PAT 21-MAR-2001
Sequence 129 from Patent WO0116318.

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Qy	961	CTCTCTATCCCTTCCCAACCTCTGATCACCTCATCTTACTCTCTACCTCCATGAGATCCAC	1020
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VERSION	AX358958.1	GI:18675380	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A., Goddard, J.P., Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P., Watanabe, C.K. and Wood, W.I. Secreted and transmembrane polypeptides and nucleic acids encoding the same		
JOURNAL	Patent: WO 0193983-A 211 13-DEC-2001;		
FEATURES	Genentech Inc. (US)		
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			Gaps 0;
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Db 361 AATTTCTCATGTATTTTCTCATTTATTTATTTTAACTGATGATGATGATGATGATGAT 420
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Db 1141 TCTTAATTTCAATTAATAAATACACACATGCGAAAAA 1177

RESULT 3
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DEFINITION Sequence 211 from Patent WO0208288.
ACCESSION AX362451
VERSION AX362451.1 GI:18694683
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
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AUTHORS Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A., Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P., Watanabe, C.K. and Wood, W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same
JOURNAL Patent: WO 0208288-A 211 31-JAN-2002; Genentech, Inc. (US)
FEATURES Location/Qualifiers
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/organism="Homo sapiens"
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ORIGIN

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Query Match 100.0%; Score 1177; DB 6; Length 1177;
Best Local Similarity 100.0%; Pred. No. 5e-275;
Matches 1177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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AUTHORS	Baker, K.P., Ferrara, N., Gerber, H., Gerttisen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J., Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I. and Ye, W.
TITLE	Compositions and methods for the diagnosis and treatment of disorders involving angiogenesis
JOURNAL	Patent: WO 0208284-A 271 31-JAN-2002; Genentech, Inc. (US); Baker, Kevin P. (US); Ferrara, Napoleone (US); Gerber, Hanspeter (US); Gerritsen, Mary E. (US); Goddard, Audrey (US); Godowski, Paul J. (US); Gurney, Austin L. (US); Hillan, Kenneth J. (US); Marsters, Scott A. (US); Pan, James (US); Paoni, Nicholas F. (US); Stephan, Jean-Philippe F. (US); Watanabe, Colin K. (US); Williams, P. Mickey (US); Wood, William I. (US)
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REFERENCE
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AUTHORS Isogai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Iehii,S.,
Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R.,
Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and
Masuho,Y.
TITLE Full-length cDNA sequences
JOURNAL Patent: EP 1347046-A 342 24-SEP-2003;
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Research Association for Biotechnology (RAB); cDNA library construction; Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- and 3'-end one pass sequencing; RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing; HRI and RAB; annotation: HRI and RAB.

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ORGANISM

REFERENCE
AUTHORS

Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 162023)
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Wlsczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J.,
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Direct Submission
Unpublished
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Direct Submission
Submitted (11-OCT-2000) Human Genome Sequencing Center, Department
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Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 162023)
Worley, K.C.
Direct Submission
Submitted (01-NOV-2001) Human Genome Sequencing Center, Department
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Baylor Plaza, Houston, TX 77030, USA
4 (bases 1 to 162023)
Worley, K.C.
Direct Submission
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5 (bases 1 to 162023)
Worley, K.C.
Direct Submission
Submitted (07-MAR-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
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6 (bases 1 to 162023)
Worley, K.C.

TITLE
JOURNAL

COMMENT

Direct Submission:
Submitted (01-OCT-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Nov 1, 2001 this sequence version replaced gi:16506862.
INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email
qc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:

STSS are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

* Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: <http://qc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html>.

Q1A1.STAT-REPORT-----

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122038	gatataaga (n) atatatatc	gatataaga (t) atatatatc
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AC027633
SEQUENCE, 12 unordered pieces.
AC027633
VERSION AC027633.2 GI:7577653
KEYWORDS HTG; HTGS PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Waterston,R.H.
1 (bases 1 to 168283)
The sequence of Homo sapiens clone
Unpublished
2 (bases 1 to 168283)
Waterston,R.H.
Direct Submission
Submitted (30-MAR-2000) Genome Sequencing Center, Washington
University School of Medicine, 444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Apr 16, 2000 this sequence version replaced gi:7344372.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H.NH0489P06
----- Summary Statistics -----
Sequencing vector: M13; 100%
Sequencing vector: plasmid; 0%
Chemistry: Dye-primer ET; 100% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 163569 bases at least Q40
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Consensus quality: 165936 bases at least Q20
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Insert size: 167183; sum-of-contigs
Quality coverage: 5.15 in Q20 bases; agarose-fp
Quality coverage: 5.15 in Q20 bases; sum-of-contigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 12 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 1385 1484: gap of unknown length
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